

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 23, 2005, 09:41:05 ; Search time 260 Seconds
(without alignments)
5588.514 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRVILNSAARG.....SICKAGESTDLSPHKLK 888

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4547	100.0	3111	4	US-09-825-147-3
3	4527.5	99.6	3137	4	US-09-590-304-1
4	4513.5	99.3	3074	4	US-09-813-148-1
5	2007.5	44.1	2335	4	US-09-492-361-1
6	1998.5	44.0	2196	4	US-09-949-016-1823
7	1794	39.5	3237	3	US-09-177-650-95
8	1792.5	39.4	3287	3	US-09-105-058C-19
9	1790.5	39.4	2169	3	US-09-105-058C-22
10	1788	39.3	3232	3	US-09-177-650-1
11	1767	38.9	2273	3	US-09-177-650-88
12	1587.5	34.9	2565	3	US-09-105-058C-26

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15	1207.5	26.6	900	3	US-09-105-058C-5	Sequence 5, Appl1
16	1201.5	26.4	900	3	US-09-105-058C-3	Sequence 3, Appl1
17	1116.5	24.6	3181	3	US-09-135-021-1	Sequence 1, Appl1
18	1116.5	24.6	3181	3	US-09-135-020-1	Sequence 1, Appl1
19	1116.5	24.6	3181	3	US-09-135-010A-1	Sequence 1, Appl1
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28	1094	24.1	2734	3	US-09-135-021-79	Sequence 79, Appl1
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34	1085	23.9	930	3	US-09-105-058C-17	Sequence 17, Appl1
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41	475	10.4	1481	4	US-09-949-016-4101	Sequence 4101, App
42	450	9.9	284	4	US-09-495-050A-304	Sequence 304, App
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44	310	6.8	1080	4	US-09-328-352-2971	Sequence 2971, App
45	260.5	5.7	1927	3	US-09-336-643A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Alignment Scores:
Pred. No.: 0
Score: 4547.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)

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DB 166 GACGGCCTCTACTCTCGGGGACACCCCGCGGCGACCTCGTGGCGGGCGGCTGGCCG 225
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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QY 121 AlaSerSerCysLeuLeuLeuGlnPheValMetIleValValPheGlyLeuGlnPhe 140
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DB 1486 TGCCAGTGTGATGTATCGATGAGAGACCTCACCCCACTTAAACCTGTACTTGGAGCT 1545
QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
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DB 1906 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATGTGCAAA 1965
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
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DB 2146 GCAGTGGAGCCACCAACACATTTGCACAAACAAATTAATATAGGCAACCAAGCCACAGCC 2205
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Qy	801	G1n1euserG1ySerG1userSerG1ySer1ySer1yArgG1ySerG1nAapPheTy1Pro1ySerTP	820
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Qy	821	ArgG1user1y1euleuPhe1le1eThrAspG1uG1uVal1G1yProG1uG1uThnG1uThnAsp	840
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Qy	861	ThrG1yAysSerAysSerSerG1nSer1leCy1a1y1a1aG1yG1userThrAsp1a1e1u	880
Db	2686	ACTGGAAGGTCAACATCATCTCAGAGCATTTGTGAAGCAGAGAAAGTAACAGATGCCCTC	2745
Qy	881	Ser1eupProH1eVal1y1e1e1y1e 888	
Db	2746	AGCTTGCTCATGTCAACTGAAA 2769	

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RESULT 2
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-3

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[illegible]

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Db	225	GACGGCCTGTACTGCTGGGCACCCGGCGCAGCTCGGGTGGCGCGCTGGCC	284
QY	41	ArgGlySerArgArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60
Db	285	AGGGAGACCCCGGGGGCAGACGGGGGCCGGATGAGCTGTGGGGAGAGCCGCTCT	344
QY	61	TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu	80
Db	345	TACACGATGACAGAGCTGCCGGCAGACGTCAAGTACCGCGGGTCCAGAACTACCTG	404
QY	81	TyrAsnValLeuGluArgProArgGlyYTrpAlaPheIleTyrHisAlaPheValPheLeu	100
Db	405	TACAAAGTGTGGAGAGACCCCGGGGCTTGCATCTACACAGCTTGGTTTTCTC	464
QY	101	LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeu	120
Db	465	CTTGCTCTTGGTGGTCTGATTTTGTCAAGTGTCTTACATCCCTGCAGACACAAATTTG	524
QY	121	AlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValIlePheGlyLeuGlnPhe	140
Db	525	GCCCTCAATGCTCTTGTGATCTTGAGTTCGATGATGTGCTGTGGTTGGATGCTTC	584
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Db	585	ATCATTCGAATCTGTGTCTGGGGTGGCTGTGTGCATTAAGATAGGCAAGAAAGACTG	644
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Db	645	AGGTTGCTCGAAAGCCCTCTGTGTGTATTAATACATTTGTTTATGCTTCATTAACA	704
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Db	705	GTTGTTTTCGAAAAACTCAGGGTAAATTTTTTGCACGTGCTGACCTAGAAAGTCCGT	764
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Db	765	TTCTTACAGATCTCTCCGATGTGTGCGATGACCGAAGGGAGACACTTGGAAATTAATG	824
QY	221	GlySerValValYTrpAlaHisSerLysGlnLeuIleThrAlaTyrPyrIleGlyPheLeu	240
Db	825	GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAAACAGCTGGTACATAGATTTTGG	884
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Db	885	GTTCTTATTTTGTGCTTCTCTGCTCATCTGTGGGAAAAAGATGCAATAAAGATTT	944
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QY	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
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QY 401 ArgArgSerProSerThrAspIleThrAlaGlyGlySerProThrIleValGlnLeuSer 420
Db 1365 AGGAGGTCCCGCAAGCAGCCGATCAGAGCCGAGGGGAGTCCCAAAATGCGAGAAAGAC 1424
QY 421 TPSPSPheAsnAspArgThrArgPheArgProSerLeuLeuGlyLeuSerGlnPro 440
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QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1725 AAAAGCCTTCAACACAGCTGTGATCAAAATCTTGGAAAAAGGCAATTCATCAGATTAAG 1784
QY 541 LysSerArgGluLysIleThrAlaGlnHisGlnThrThrAspAspLeuSerMetLeuGly 560
Db 1785 AAGAGCCGAGAAATTAACAGCAACATGAAACCAACAGATTCATGATTCGCTGCT 1844
QY 561 ArgValIleLysValGlnLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeu 580
Db 1845 CCGGTGTCAAGGTTGAAAAACAGTACAGTCAATGAAATTCAGAGCTGAGCTCCACTA 1904
QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1905 GACATCTATCAACAGAGCTCTTCGAAAGGCTCTGCTCAGCCCTCCCTTGGCTTCATTC 1964
QY 601 GlnIleProProPheGlnCysGlnGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1965 CAGATCCCACTTTTAAATGTGAACAGACATCTGATTCAAAGCCCTGTGATAGCAAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 2025 GATCTTTCCGGGTTCCGCAAAAACAGTGGCTGTTTCCAGATCAACTGATGCAAAACAT 2084
QY 641 SerArgGlyLeuGlnIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAla 660
Db 2085 TCGAGAGGGCTGCAAGTTCATCTGAGCCAAATGAACTTCAAGGCCCACTTCTCAACGG 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2145 CTTAAGCCCTACTATGACAGTCAAGCAACAGAGTCCCAATTTGTCAAAGCCATGGCTCA 2204
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2205 GCAAGTGGCAGCCCAACACCAATTCGCAAACTAAATACGGCAACCCAAAGCCAGAGCC 2264
QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2265 CCAACAACTTTACAGATCCCACTCTCTCCAGCAGCATCAACATCTGCGCAGGCCAGAA 2324
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740
Db 2325 ACTCTGCACCCCTAACCCCTGACGGCTTACAGAAAGCAATTTCTGACGTCACCACTGCTT 2384

QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2385 GTTCCTCCAAAGAAATGTTCAAGTTGCACAGTCAAAATCTCACCAAGACCGTTCTATG 2444
QY 761 ArgLysSerPheAspMetGlyGlyGlnThrLeuLeuSerValCysProMetValProLys 780
Db 2445 AGGAAACCTTTGACATGAGAGGAGAACTCTGTTGTCTGTCTGTCCATGGTGTCCGAAG 2504
QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleAsnSerThrGlnGlnLeuAsnIle 800
Db 2505 GACTTGGCAATCTTTGTCTGTGCAAAACCTGATCAGTGCAGCCGAGAACTGAATATA 2564
QY 801 GlnLeuSerGlySerGlnSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
Db 2565 CAACCTTCAGGAGAGTGAAGTCAAGTGTCCAGAGCCAGCAAGATTTTACCCCAATCG 2624
QY 821 ArgGlnSerLysLeuPheIleThrAspGlnGlnValGlyProGlnGlnThrGlnThrAsp 840
Db 2625 AGGGAATCCAAATTTGTTATATGATGAAAGAGTGTCCCGAAGACAGACAGACAG 2684
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGlnAlaAlaPheAlaSerAspSerLeuArg 860
Db 2685 ACTTTGATGCCGACACCGCAGCTGTCCAGGAAGCTGCTTTGCATCAGACTCTTAAG 2744
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGlnSerThrAspAlaLeu 880
Db 2745 ACTGGAAGTCAACGATCATCTCAGAGCATTTGTAAAGCAGAGAAAGATACAGATCCCTC 2804
QY 881 SerLeuProHisValLysLeuLys 888
Db 2805 AGCTTGCTCATGTCAAACTGAAA 2828

RESULT 3
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590.304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2691)
US-09-590-304-1

Alignment Scores:
Pred. No.: 0 Length: 3137
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 99.57% Indels: 9
DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x US-09-590-304-1 (1-3137)

QY 1 MetLysAspValGlnSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaIleArgGly 20
Db 1 ATGAAGAGTGTGGAGTCCGGCCCGGGGCGAGGTGCTGCTGAATCTGGCAGCCCGGGGGC 60
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlnGlyGlyGlyGlyLeu 40
Db 61 GACGGCTGTACTAGCTGCTGGGACCCGGCGGCGCAAGCTCGGTGGGGGGGGTGGCTTG 120
QY 41 ArgGlnSerArgArgGlyLysGlnGlnIleAlaArgMetSerLeuLeuGlyLysProLeuSer 60


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Db 121 AGGAGAGCGCGGGGAGAGAGAGGGCGCGGATGAGCTGCTGGGAGAACCGGCTCTCT 180
Qy 61 TyrThrSerSerGlnSerCybArgArgAsnValIlySerYArgArgValGlnAsnTrpLeu 80
Db 181 TACACGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 81 TyrAsnValIleuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACACGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 101 LeuValPheGlyCybLeuIleLeuSerValPheSerThrIleProGlnHisTrpLeu 120
Db 301 CTGTGCTTGGCTGATTTTGTGAGTGTCTTTTCTACCATCCCTGAGCACAAGAAATTG 360
Qy 121 AlaSerSerCybLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTTGCTCTTGATCTGAGATTGCTGATGATTGCTCTTTGGTTGGAGTTTC 420
Qy 141 IleIleArgIleTrpSerAlaGlyCybCybArgTrpArgIleTrpGlnIleArgLeu 160
Db 421 ATCATTCGAAATCTGGTCTGGGGTGTCTGTGTGATATGAGAGATGGCAGAGAGAGCTG 480
Qy 161 ArgPheAlaArgIlySerProPheCybValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTTGCTGAGAAAGCCCTTCTGTGTTATGATACCATTTGTTCTTATCCGCTTCAATAGCA 540
Qy 181 ValValSerAlaIlySerThrGlnIlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTTCTGCAAAAATCTCAGGGTAATATTTTGGCCAGTCTGACACTCAGAAAGTCCCT 600
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgIlyGlnIlyTrpIlySerLeu 220
Db 601 TTCTTCAGATCTCCGATGAGTGGCAGATGACCAAGAGGAGAGACTTGGAAATATCTG 660
Qy 221 GlySerValValIlyAlaHisSerIlyGluLeuIleThrAlaTrpIlyIleGlyPheLeu 240
Db 661 GGTTCAGTGGTTATGCTCAGACAGAGATTAATCAGCTTGATACATAGAGATTTTTC 720
Qy 241 ValLeuIlePheSerSerPheLeuValIlyLeuValGluIlyAspAlaAsnIlyGluPhe 260
Db 721 GTTCTTAATTTTTCGCTTTCCTTGTCTATCTGTGTGAAAAGATGCAATAAAGAGTTT 780
Qy 261 SerThrTrpAlaAspAlaLeuTrpIleGlyThrIleThrLeuThrIleGlyTrpIly 280
Db 781 TCTACATATGCAATGCTCTCTGTGTGGGACAAATTAATTAATTAATTAATTAATTAATTA 840
Qy 281 AspIlyThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 841 GACAAAACCTCCCTTAATCTGCTGGGAGATTCCTTTCTGCAAGCTTTGCACTCTTGCG 960
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuIlyValGln 320
Db 901 ATTTCTTTCTTTCCTGCTCTGCGGATTCCTTGCTCAGTTTTCATTAATAAGATCA 960
Qy 321 GluGlnHisArgGlnIlyHisPheGluIlyArgArgAsnProAlaIleAsnLeuIleGln 340
Db 961 GAAACAACCGGACAGAAACCTTTGAGAAAGAGAGAACCCAGCTGCAACCTCATTCAG 1020
Qy 341 CybValTrpArgSerTrpAlaAlaAspGluIlySerValSerIleAlaThrTrpIlyPro 360
Db 1021 TGTGTTTGGGTGATTACGCAAGCTGATGAGAAATCTGTTTTCATTCGAACCTGGAAGCCA 1080
Qy 361 HisLeuIlyAlaLeuHisTrpCybSerProThr----- 371
Db 1081 CACTTAAAGGCTTTCACACCTCAGCCCTTACCAAGAAAGAACAGAGGAGCATCAAG 1140
Qy 372 AsnGlnIlyLeuSerPheIlyGluArgValArgMetAlaSerProArgIlyGlnSerIle 391
Db 1141 AGTCAGAGAGTAAATTTTAAAGAGAGAGTGCATGCTAGCCCAAGGGGCCAGAGTATT 1200
Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db 1201 AAGAGCCGACAAGACCTCAGTAGGTGACAGAGGTCCCAAGCACCGCATCAAGCCGAG 1260
Qy 412 GlySerProThrIlyValGlnIlySerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1261 GGCAGTCCCAACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
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Qy 452 ThrAspAspValIlyTrpAspGluIlyGlyCybGlnCybAspValSerValGluAspLeuThr 471
Db 1381 ACTGATGATGATATATGATGATAAAGATGCCAGTGTGATGATGATGATGATGATGATGAT 1440
Qy 472 ProProLeuIlySerThrValIleArgAlaIleArgIleMetIlyPheHisValAlaIlyArg 491
Db 1441 CCACCACTTAAACCTGCTATGAGCTTACAGATTAACAAGATTAATAATTCATCTTCCAAAACGG 1500
Qy 492 LysPheIlyGluThrLeuArgProIlyAspValIleGluGlnIlyTrpSerAla 511
Db 1501 AAGTTTAAGAGAAACATTAAGCTCATTGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 512 GlyHisLeuAspMetLeuCybArgIleIlySerLeuGlnIlyArgValAspGlnIleLeu 531
Db 1561 GGTCACTGAGACATGTTGTGTAATTAAGCTTCAAAACAGTGTGATCAAAATTTCTT 1620
Qy 532 GlyIlyGlyGlnIleThrSerAspIlySerArgGluIlyGlnIleThrAlaGlnHisGlu 551
Db 1621 GGAAAAGGGCAATCAATCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValIleIlyValGluIlyGlnIlyGlnSer 571
Db 1681 ACCACAGAGATCTCAGTATGCTCGGTGGGTGTGTCAGAGTTGAAAACAGATACAGTCTC 1740
Qy 572 IleGluSerIlyLeuAspCybLeuLeuAspIleIlyGlnGlnValLeuArgIlyGlySer 591
Db 1741 ATGAAATCCAGCTGAGCTGCTTACATCAAGATCTTCAACAGAGTCTTGGAAAGCTCT 1800
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluIlyGluGlnIlyThrSer 611
Db 1801 GCCTCAGCCCTGCTTGGCTTTCATTCAGATCCCACTTTGAAAGTGAACAGACATCT 1860
Qy 612 AspIlyGlnSerProValAspSerIlyAspLeuSerGlySerAlaGlnAsnSerGlyCyb 631
Db 1861 GACTATCAAGCCCTGTGATAGCAAAAGTCTTTGGGGTCCGACAAAACAGTGTCTC 1920
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgIlyLeuGlnPheIleLeuThrProAsn 651
Db 1921 TTATCCAGATCAACTAGTCCAAATCTCGAGAGGCTGCACTTCTGACGCCAAAT 1980
Qy 652 GluPheSerAlaGlnThrPheTrpAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1981 GAGTTCAGGCCCAAGCTTTCATACGCGCTTACCCCTTACATCAAGTCAACCAACACAG 2040
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
Db 2041 GTGCCAATTAATGCAAAAGCATGCTCAGCAGTGGAGCCACCAACCACTTGGCAACCA 2100
Qy 692 IleAsnThrAlaProIlySerProAlaAlaProThrTrpLeuGlnIleProProProLeuPro 711
Db 2101 ATTAATACGGCAACCAAGCAGACAGCCCAACCACTTACATGATCCACCTCTCTCCCA 2160
Qy 712 AlaIleIlyHisLeuProArgProGluTrpLeuHisProAsnProAlaGlyLeuGlnIly 731
Db 2161 GCATTCACAGCATCTGCCAGGCAAGAACTTCGACCCCTTAACCTTCAGAGCTTAAAGGAA 2220
Qy 732 SerIleSerAspValIlyThrCybLeuValAlaSerIlyGluAsnValGlnValAlaGln 751
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Qy 752 SerAsnLeuThrLysAspArgSerMetArgIlySerPheAspMetGlyIlyGluTrpLeu 771
Db 2281 TCAAAATCTCAACAGAGACGTTCTATGAGAGAAACCTTGAATGATGAGAGAGAAACTCTG 2340
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QY 772 LeuSerValCyseProMetValProLyAspLeuGlyLyseSerLeuSerValGlnAsnLeu 791
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Db 2341 TTGTCTGTCTGTCCTCCATGGTGGCGAAGGACTTGGCGAAATCTTTGTCTGTGCAAAACCTG 2400
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QY 792 TLeaYSerThrGlnGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
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Db 2401 ATCAGGTTCACCGAGAACCTGATATACACTTTCGGAGGTGAGTCAAGTGGCTCCACA 2460
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QY 812 GlySerGlnAspPheThrProLySerTrpArgGluSerLeuPheIleThrAspGlnGlu 831
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Db 2461 GGCAGCGCAAGATTTTATCCCAATATGAGGAAATCCAAATGTTTATATCATGATGAAG 2520
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|
QY 832 ValGlyProGlnGluThrGlnThrAspThrPheAspAlaIleProGlnProIleArgGlu 851
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Db 2521 GTGGGTCCCGAAGACAGACAGACACTTTTGTGATCCGACCGCAGCCTCCAGAGGA 2580
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QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
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Db 2581 GGTGCTTTGACATCAGACTCTCTTAAGAGCTGAAGGTCAAGTCAATCTAGAGCAATTGT 2640
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QY 872 LySAlaGlyGluSerThrAspAlaLeuSerLeuProHleValLyseLeuLys 888
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Db 2641 AAGCGAGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAAACTGAAA 2691
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RESULT 4
US-09-813-148-1
/ Sequence 1, Application US/09813148
/ Patent No. 6617131
/ GENERAL INFORMATION:
/ APPLICANT: STEINMEYER, Klaus
/ APPLICANT: LERCHE, Christian
/ APPLICANT: SCHERER, Constanze
/ APPLICANT: SEEBOW, Guiscard
/ APPLICANT: BUSCH, Andreas E.
/ TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CEN
/ TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
/ FILE REFERENCE: 38005-119
/ CURRENT APPLICATION NUMBER: US/09/813,148
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: DE 100 13 732.6
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/194,041
/ PRIOR FILING DATE: 2000-04-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-813-148-1

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

QY 61 TyrThrSerSerGlnSerCysArgHisAnValLysTyrArgArgValGlnAsnTyrLeu 80
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Db 395 TACAGAGATGACGACAGAGCTGCGGCGCAACGTCAAGTACCGCGGCTGCAGAACTACCTG 454
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|
QY 81 TyrAsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
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|
|
Db 455 TACACGCTGCGAGAGACCCCGCGGCTGGCTTCATCTCCACAGCTTTCGTTTCTCTC 514
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QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHleThrLysLeu 120
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|
Db 515 CTGTGCTTGGTGTGCTTAATTTTGTCACTGTTTCTACATCCCTGAGACACAAATTTG 574
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QY 121 AlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValIlePheGlyLeuGlnPhe 140
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Db 575 GCCTCAAGTGGCTCTTGATCTCGAGATTCGAGATTTGTCGATGTTGCTTGGTGAAGTTG 634
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QY 141 TleIleArgIleTyrPheSerAlaGlyCysArgCysArgTyrArgGlyTyrGlnGlyArgLeu 160
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Db 635 ATCATTCGAATCTGGTCTGGCGGTTGCTGTTGTCATATAGAGATGGCAAGAAAGACTG 694
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QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla 180
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Db 695 AGGTTTGTCCAAAGCCCTTCTGTGTTATAGATACATTTGTTTATGCTTCAATACCA 754
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QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrThrTyrLysLeu 220
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QY 815 TTCTTACAGATCTTCGGATGATGGCGCATGGACCGAAGGAGGACTTGAATAATCTAG 874
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QY 221 GlySerValValTyrAlaHleSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
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Db 875 GGTTCAAGTGTATATGCTCACAGCAAGAAATTAATCACAGCTTGGTATAGATTTTGG 934
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QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGlyLysAspAlaAsnLysGluPhe 260
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Db 935 GTTCTTATTTTTCGTCCTTCTTCCTGTCATCTGGTGCAAAAGATTAAGTAAAGTTT 994
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QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
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Db 995 TCTACATATGCAAGATGCTCTCGTGGGGCAAAATTAATTAATGACATATGCTATAGGA 1054
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QY 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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QY 301 TLeSerPhePheAlaLeuProAlaGlyTyrLeuGlySerGlyPheAlaLeuLysValGln 320
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QY 321 GlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAlaAsnLeuIleGln 340
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Db 1175 GAACACACCCCGCAGAAACACTTTGAGAAAGAAAGAAACCAAGCTCCCACTCAATTAG 1234
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QY 341 CysValTyrPArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTyrLysPro 360
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Db 1235 TGTGTTTGGCGTAAAGTTAAGCACTGATGAGAAATCTGTTTCCATTGCAACTGGAAAGCCA 1294
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QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
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Db 1295 CACTTGAAGGCTTTCGACACCTGAGCCCTTACCAAGAAAGCAAGGGAAGCATCAAGC 1354
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|
QY 372 AsnGlnLysLeuSerPheLysGlnArgValArgMetAlaSerProArgGlyGlnSerIle 391
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|
Db 1355 AGTCAGAAAGCTTAAGTTTAAAGAGGAGGTGCAAGTGTACCCAGGAGGCAAGATTT 1414
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|
QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGln 411
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|
Db 1415 AAGAGCGAGCAAGGCTCATGTAAGTGAACGAGAGTCCCAACACCGAATCATCACGCCAG 1474
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QY 412 GlysSerProThrIysValGlnIysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
 Db 1475 GGCAGTCCCAAGAGGAGGAGAGGAGCTGGAGCTTCAACGACCGACCTCCGGCCC 1534
 QY 432 SerLeuArgLeuIysSerSerGlnProIysProValIleAspAlaAspThrAlaLeuGly 451
 Db 1535 TCCCTGGCCCTCAAAAGTTCTCAGCCCAAAACAGTGTATGATCTGCACACGCTTCGGC 1594
 QY 452 ThrAspAspValIyrAspGluIysGluIysGluIysGluIysGluIysGluIysGluIys 471
 Db 1595 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1654
 QY 472 ProProLeuIysThrValIleArgAlaIleArgIleMetIysPheHisValAlaIysArg 491
 Db 1655 CCACCACTTAAACCTGCTATTCGAGCTATCAGAAATTATGAATTCTCATGTTGCAAAACGG 1714
 QY 492 LysPheIysGluThrLeuArgProIyrAspValIysAspValIleGluGlnIyrSerAla 511
 Db 1715 AACGTTAAGGAAACATTACCTCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1774
 QY 512 GlnHisLeuAspMetLeuIysArgGluIysSerLeuGlnIyrArgValAspGlnIleIeu 531
 Db 1775 GGCATCTGGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1834
 QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluIysIleThrAlaGluHisGlu 551
 Db 1835 GGAAGAGGCAATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1894
 QY 552 ThrThrAspAspLeuSerMetLeuGluIysArgValIysValIysGluIysGlnIys 571
 Db 1895 ACCACAGACGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1954
 QY 572 IleGluSerIyrLeuAspCysLeuLeuAspIleIyrGlnGlnIyrAlaLeuArgLysSer 591
 Db 1955 ATGAAATCCAGGCTGGAGCTGCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 2014
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnIyrSer 611
 Db 2015 GCCTCAGCCCTGCTTGGCTTTCATTCGATCCGATCCGACCTTTGAATGTGAACGACATCT 2074
 QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 2075 GACTATCAAAAGCCCTGTGATCAAAAGATCTTCCGGGTTCCCAACAAACATGGCTGC 2134
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleuThrProAsn 651
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 QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 2195 GAGTTCAAGTCCCAAGACTTTCTACGGCTTACGCCCTCATGATGACAGTCAAGCAACACAG 2254
 QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
 Db 2255 GTGCCAATTAGTCAAAAGCGATGCTCAGAGTGGAGCCCAACCAACCATTCGCAACCA 2314
 QY 692 IleAsnThrAlaProIysProAlaIleProThrThrLeuGlnIleProProPheLeuPro 711
 Db 2315 ATAAATACGGACCCCAAGCAGACGCCCAACCACTTACAGATCCACACTCTCTCCCA 2374
 QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
 Db 2375 GCATCATAGATCTGGCCAGGCGCAAAACCTCTGCAACCTTACAGCTTACAGGAA 2434
 QY 732 SerIleSerAspValIThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
 Db 2435 AGCATTTCTGACGTCACACCTGCTTGTTCCTCCCAAGGAAATGTTCCAGGTTCACAG 2494
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 Db 2495 TCAAACTTCAACCAAGGACGCTTCTATGAGAAAGCTTTGACATGGAGAGGAAACCTCTG 2554
 QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791

Db 2555 TTGTCTGTCTGTCCCATGGTGCAGAGGACTTGGGAAATCTTTGCTGTGCAAAACCTG 2614
 QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
 Db 2615 ATCAGGTTCACCGAGGAACTGATATATACACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674
 QY 812 GlysSerGlnAspPheTyrProIysTrpArgLysSerLysLeuPheIleThrAspGluGlu 831
 Db 2675 GGCAGCCAAATTTTATCCCAATGAGAGGAAATCCAAATTTGTTTATCTGATGAAGAG 2734
 QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 851
 Db 2735 GTGGGTCCCGAGAGACAGACAGACACTTTTGAATGCCGACCCGACGCTCGCAGGAA 2794
 QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
 Db 2795 GCTGCCCTTTCATCAGACCTCTTAAGGACTGGAAGTCAAGATCAATCTCAGAGCATTTGT 2854
 QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValIysLeuLys 888
 Db 2855 AAGCAGGAAAGTACAGATGCCCTTCAGCTTGCCTCATGTCAAACTGAAA 2905
 Db 2855 AAGCAGGAAAGTACAGATGCCCTTCAGCTTGCCTCATGTCAAACTGAAA 2905
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 US-09-492-361-1
 ; Sequence 1, Application US/09492361
 ; Patent No. 6794161
 ; GENERAL INFORMATION:
 ; APPLICANT: JENTSCH, Thomas J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
 ; FILE REFERENCE: 2815-127P
 ; CURRENT APPLICATION NUMBER: US/09/492,361
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2335
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: gene
 ; LOCATION: (1)..(2335)
 ; NAME/KEY: CDS
 ; LOCATION: (83)..(2170)
 US-09-492-361-1
 Alignment Scores:
 Pred. No.: 2335
 Score: 5.98e-203
 Percent Similarity: 2007.50
 Best Local Similarity: 65.328
 Query Match: 54.948
 DB: 44.15#
 Gaps: 16
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 QY 8 ArgGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGlyLeuLeuLeuLeuGly 27
 Db 127 CGGGAGCGCCCGCCGCGAGCTAGTGGCTCAGGC----- 165
 QY 28 ThrArgAlaAlaThrLeuGluGlyGlyGlyGlyLeuArgGluSerArgArgGlyLys 47
 Db 166 ---CGTCAAGACGAACAGGCGGAGCGG-----CGGGGCGG 201
 QY 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
 Db 202 CTCGCCGCGCGCTCCTGAGCTCTGAGGACGCCCTCGCGCGCGGCGGCCCTCCTGG 261
 QY 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValLysTyr 73
 Db 262 GCGGGGCTCCGGCTCGGGCTCGGCTCGGCGGCGGCTTCCTGGCGCGGACAGACGCTTA 321

OY		73	AATGAGTAAAGTAAGTAAATCTTTGGTGTCTTCAGTGCGCTGGAGCTGTCTGACGAGTGAATTCGATGAT	501
Dp		322	CCGCCGCTGCAGAACCTGGATTACCAAGTGTGAGAGGCCCCCGGCTGGGCTTGT	381
OY		93	eTYrHisAlaPheValPheLeuLeuValPheGLyCysIleuIleLeuSerValPheSerTh	113
Dp		382	CTACCAGCTTCATCATTTTTTGGTGTCTTCAGTGCGCTGGAGCTGTCTGACGAGTGAATTCGATGAT	441
OY		113	rILeProGluHisThrLysIleuAlaSerSerCysIleuLeuIleLeuGluPheValMetI	133
Dp		442	TATCCAGAGACAACAGAACTTGCACACGAGGTCTCTCATCTTGGAAATTCGATGAT	501
OY		133	eValValPheGlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTy	153
Dp		502	CCTGGTTTCCGCTTGGAGTACATGTCGGGTCTGATCCCGGATGCTCTGCTGCCGCTA	561
OY		153	rARGLyITrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI	173
Dp		562	CCGAGGAAGGAGAGGTCCCTTCCTCCGCTTGGCCAGAAAGCCCTTGTGTGCATCGACTCAT	621
OY		173	eValIleuIleAlaSerIleAlaValIleSerAlaLysThrGlnGlyAsnIlePheAlaTh	193
Dp		622	CGTGTTCGTGGCTTCGTGGTCCGTATGCGCGGGGTACCCAGGCAACATCTTCCGAC	681
OY		193	rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr	213
Dp		682	GTCGCGCGCTGGAGCATGCCCTTCTCAAGATCCTGGCATGTGGCCCATGACCCGCG	741
OY		213	ggIGlYrHrTrpLysIleuLeuGlySerValValTrpAlaHisSerLysGluLeuIleTh	233
Dp		742	CGGCGGCACTGGAGAAGCTGTGGGTCTCAGTGGTCTCACCGGCATGCCAAGAGACTGATAC	801
OY		233	rAlaTrpTrpIleGlyPheLeuValIleuIlePheSerSerPheLeuValTyLeuValGI	253
Dp		802	CGCCGTGATACATCGGATTCCTGGTCTCATCTTCGCTTCCTTCGATCTACCTGGCGGA	861
OY		253	uLYaAspAlaAsnLysGluPheSerThrTyAlaAspAlaLeuTPTrpGlyThrIleTh	273
Dp		862	GAAAGACCCCAACTCCGACTTCTCTCTACGCCCACATCGCTGTGGGGGAGCATTAAC	921
OY		273	rLeuThrThrIleGlyTyrgLyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSe	293
Dp		922	ATTGACAAACATCCGCTATGTGTGACAAACACCCGACACATGTGGCTGGGCAAGGTCCTGGC	981
OY		293	rAlaGlyPheAlaLeuLeuGlyLysIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe	313
Dp		982	TGCTGGCTTCCTCCCTTACGTGGGATCTCTTCTTGGCTCCGTGGCGGATCTTAGGCTC	1041
OY		313	rGlYPheAlaLeuLysValGlnGluGlnHisArgGlnLysHisPheGlyuLYaAspArgAs	333
Dp		1042	CGGCTTTCCTGAAAGTCCAGAGACACACCGGAGAAACATTCGAAAGCCGAGGAT	1101
OY		333	nProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrrAlaAlaAsp---GluLysSe	352
Dp		1102	GCCGGAGCCCAACTCATCCAGAGCTGTGGGCGCTGATCTCACCCGATTAGAGCCGGGC	1161
OY		352	rValSerIleAlaThrTrp-----	358
Dp		1162	CTACCTGACACCACTGGTACTACTATGACAGTATCTCTCCATCTTCAGAGAGCTGGC	1221
OY		358	-----	358
Dp		1222	CCTCTTGTTTAGACACGTGCAAACGGGCGCCGCAATGGGGGCGCTACGGCCCTCGAGAGTGGC	1281
OY		359	-----LysProHisLeuLysValAlaLeuHisTh	367
Dp		1282	GCGGAGCGCGGTACCCGACGAGCACCTCCCGTTACCCGCGCGTGGCCACTGCGACCG	1341
OY		367	r-----CysSerProThAsnGlnLysLeuSerPheLysGluArgVa	381
Dp		1342	GCCGGGACGACACTCTTCTCTCCCTCGGGGAAAAGCAGCCGAGATGGGACATCAAAAGCCGAT	1401
OY		381	LArgMetaLaserProArgGlnSerIleLysSerArgIn-----AlaSerValGI	399

Db	1402	CCGCAATGGGACAGCTCCCAAGCGGCGGAGGGCTCTTCCAAAGCAGACGCTGGCACTCCAC	1461
Qy	399	YASpARgYgSerProSerThraPILeThraIagUgly--SerProThrlYsValGI	418
Db	1462	AATCCCCCACTCCCCCAAGCAGCGAGCGAGGAGGAGGAGCCACCAAGCCCCCAAGAGTGCA	1521
Qy	418	nlySerSerThrsrPhehAnAPaTgThraTgPhePheAryProSerleuThrlYeuYssrse	438
Db	1522	AAAGAGCTGGAGCTTCATGACCGCACCCGCTTCGGGCACTCTTGAGACTC-----	1573
Qy	438	rGlnProLyPProValIleAspAlaPThraIaLeuGIYThraSpaPValYraPgi	458
Db	1574	-----AAACCCCGCACTCTGAGGAGATGCC---CCCTCAGAGAGATGACAGAGA	1623
Qy	458	uLygLIyGsgInCySaPValSerValGIuAspLeuThrProProleuYgThrlI	478
Db	1624	GAAAGAGCTACAGAGTGAGCTCAGCGTGAGACAGCATATCGCTGTGAAGACATCAT	1683
Qy	478	eARgAlaIleArgIleMeLySPheHsValAlaYsArgYpHeLygLIuThrlEuAr	498
Db	1684	CCGCTCCATCAGATTCCTCAAGTTCCTGCTGGCCAAAGAAATTCAGAGAGACACTGCG	1743
Qy	498	gProTyThraPValIySaPValIleGIuGInTySerAlaGIYHIsleuAspMeLLeuCy	518
Db	1744	ACCGTACGACCTGAGAGACGTCATGTGACAGTACTCAGCAGGCCACTTGACAGCTGGG	1803
Qy	518	sARgIleLySerleuGInThraTgValaAPGInIleuGIYLygLIyGInIleThrse	538
Db	1804	CCGATTCAGAGCCTCGCAACTCGGGTGGACCAAAATGTGGGTGGGGG-----CCCGG	1857
Qy	538	rAspLyLySerArygLIu-----LyrlleThraIagLIuHIsGIuThrThraPaS	555
Db	1858	GGAAGAGAGGCGCCGGAGAAAGGGCGCAAGAGGGCCCTCCGACCGGAGGTGGTGATGA	1917
Qy	555	pLeuSerMeLleuGIYrYgValYValYsValGIuYsGIuValGIserIleGIuSerly	575
Db	1918	AATCAGCATGTATGGGACCGCTGGTCAGAGTGAGAAACAGAGTGAGTCCATCGAGCAAA	1977
Qy	575	sIleuAspCySleuLeuAspIleTyrgInGIuValIleuArgYLeuGIYSerAlaSerAlaIe	595
Db	1978	GCTGAGACTGCTGTGGAGCTTCATTCGCGCTGCTGCGCTCGGCACTCGGCGC-----	2032
Qy	595	uAlaLeuAlaSerPheGInIleProProPheGIuCyGsgInGIuThrSerApyrGIuSe	615
Db	2033	-AGCTGGGCGCCCTGGAGAGGCGCGTGTTCGACCCGCAATCATCCTTCAGATCACAG	2091
Qy	615	rProValAspSerTyAspLeuSerGIYSerAlaGIuAspSerGIYCySleuSerArySe	635
Db	2092	CCCTGTGGACACAGAGACATCTCCGTCTCGCACACACCTCAGC--ATCTCCGCTC	2148
Qy	635	rThSerAlaAsnIleSerArgIlyLeuGIuPheIleuThrProAsnGIuPheSerAl	655
Db	2149	GGTCAGACACCAACTGACTGAGGG-----	2173
Qy	655	agInThrPheYrIlaLeuSerProThrMeHIsSerGIuAlaThrGIuValProIleSe	675
Db	2174	-----ACTTC	2178
Qy	675	rGlnSerAspGIYSerAlaValAlaIaThraSnrThrlleAlaAsnGIuIleAsnThraI	695
Db	2179	TCAGAGGAGGAGGAGCA-----CGGCAGC	2205
Qy	695	aProLyPProAlaIaProThrThrlEu-GlnIleProProProleuProAlaIeYsH	715
Db	2206	CCCCGGCGTGGCGCTCGCACTGCCCTCTAGAGCTTCGAGTCTCTGATCTTGAACCT	2265
Qy	715	IseuProArygProGIuThrlEuHIs	723
Db	2266	CACCTCCCTCAGCGGAGAGAGACAC	2291

Db	1687	CGGGTGGACCAAAATTTGGTGGGCGG-----CCCGGGAGACAGGAAGCCCGGAGAG	1740
Qy	545	-----LysIleThrAlaGlnHisGluThrThrAspLeuSerMetLeuGlyArgVal	562
Db	1741	GGCGACAAAGGGGCGCTCCGACCGCGAGGTGGTGAATGAATACGATGATGAGACGCGTG	1800
Qy	563	ValIysValGluIlyGlnValGlnSerIleGluSerIlyLeuAspCysLeuLeuAspIle	582
Db	1801	GTCAAAGGTGGAGAAACAGAGTGCAGTCCATTCGAGCAACAGCTGGACCTCTGTGGCTTC	1866
Qy	583	TyrGlnGlnValLeuArgIlyGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIle	602
Db	1861	TATTCGCGCTGCTGCTGCTGCTGGACCTCGGCC-----AGCTGGGCGCGCTGCAAGTG	1914
Qy	603	ProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerIlyAspLeu	622
Db	1915	CCGCTGTTTCGACCCCGACATCACCCTCCGACTACACACACCCCTGTGTGACACAGAGCAATC	1974
Qy	623	SerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArg	642
Db	1975	TCCGCTCTCCGACACAGACCGCTCAGC--ATCTCCCGCTGGTCCAGCACCAACATGACTGA	2031
Qy	643	GlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSer	662
Db	2032	GGG-----	2034
Qy	663	ProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaVal	682
Db	2035	-----ACTTCTCAGAGGACAGGACAGCA---	2056
Qy	683	AlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProIlyProAlaAlaProThr	702
Db	2059	-----CGGCGACGCCCGCGCGCTGGCGCTCCGACT	2088
Qy	703	ThrIleu-GlnIleProProleuProAlaIleIlyHisIleuProArgProGluThrIle	722
Db	2089	GCCCTTCGAGGCTCCGAGCTCTCTGTACTGAATCACTCCTCAACGAGGAGAGAGA	2148
Qy	722	uHis 723	
Db	2149	CCAC 2152	
RESULT 7			
US-09-177-650-95			
: Sequence 95, Application US/09177650			
: Patent No. 6413719			
: GENERAL INFORMATION:			
: APPLICANT: Lepreert, Mark F.			
: APPLICANT: Singh, Nanda			
: TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE			
: TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)			
: FILE REFERENCE: 2323-134			
: CURRENT APPLICATION NUMBER: US/09/177,650			
: CURRENT FILING DATE: 1998-10-23			
: EARLIER APPLICATION NUMBER: 60/063,147			
: EARLIER FILING DATE: 1997-10-24			
: NUMBER OF SEQ ID NOS: 129			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 95			
: LENGTH: 3237			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (128)..(2917)			
US-09-177-650-95			
Alignment Scores:			
Pred. No.:		6,32e-180	Length: 3237
Score:		1794.00	Matches: 432

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Qy 360 -----ProIleLeuYalaLeuHISThr ----- 367
Db 1259 ACCTAGGGGGCTCCAGACTTATCCCGCTGAACACAGCTGAGCTGAGAAACTTC 1318
Qy 367 ----- 367
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Qy 368 -----CysSerPro-----ThrAngIleuLeu 375
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Qy 376 SerPheIleuValArgMetAlaSerProArgGlyIleSerIleYserArgGln 395
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Qy 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGlyIleSer 413
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Qy 414 ProThrIleValGlnIleYserTrpSerPheAsnAspArgThrArgPheArgProSerIleu 433
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Qy 434 ArgLeuIleYserSerGlnProIleValAlaAspAlaSerThrAlaLeuGlyThrAsp 453
Db 1616 CGCATCAAGGCTGCCCGGTACCGGCAACTCAGAA---GAGCAGAGCTCCCGGAGAG 1672
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Db 1673 GACATTTGTGATGACAAAGACTGCTCCCTCGAGATTGTGACCGAGGACCTGAGCCCGGGC 1732
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Db 1733 CTCAAGATCAGATCAAGCGCGTGTGTGATGCGGTCTGTGATGTCAGAGCGGAAGTTC 1792
Qy 494 LysGluThrLeuArgProIleArgValIleAspValIleGluGlnIleYserAlaGlyHIS 513
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Qy 534 GlyGlnIleThrSerAspIleYserArgGluIleThrAlaGluHISGlyIleThr 553
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Qy 554 AspAspLeuSerMetLeuGlyArgValIleIleValGluIleGlnIleGlnIleGlu 573
Db 1970 GAGGAGCCCGGACGATGAGGACCGCTCGGAGAGGTGAGAGAGAGCTTGTCTCATGAG 2029
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Qy 594 AlaLeuAlaLeuAlaSerPheGlnIleProProPheGlyCys----- 607
Db 2075 -----ATCCCGCCGACAGAGCCGAGGCTTACTTTGGGGCC 2110
Qy 608 -----GluGlnThrSerAspIleYrGlnIleProValAspSerIleYsAspLeuSerGly 624
Db 2111 AAGAGCCCGGAGCGGCGCGGTACCAAGCCCGGAACAGCCGGAGG----- 2161
Qy 625 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 644
Db 2162 CATGTGACAGGACGCGTGTGATGTCAAGATGTCGCGCTCCAGAGCTCCAGCGGC--- 2218

Qy 645 GlnPheIleLeuThrProAngIlePheSerAlaGlnThrPheThrAlaLeuSerProThr 664
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Qy 665 MetHISerGlnAlaThrGlnValProIleSerGlnIleAspGlySerAlaValAla 684
Db 2218 ----- 2218
Qy 685 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProIleProAlaIleProThrIleu 704
Db 2219 -----CAGAGAACTTCTCGCGCCCGCCGCGCGCC---CCTGTC 2257
Qy 705 GlnIleProPro-----ProIleProAlaIleIleHIS 715
Db 2258 CAGTGTCCGCTCCACCTCTCGGACGACAGAGCCACCCGCG---CCAGGCGCACGGCAC 2316
Qy 716 LeuProArg-----ProGluThr-----LeuHIS-ProAsnProAlaGlyLeuGlnI 731
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Qy 731 uSerIleSerAspValIleThrCysLeuValAlaSerIleYsGluAsnValGlnValAla 751
Db 2377 GTGCGTGTCCGCTACAGCGGGGCAACCGCGCAGCATGAGTTCTCGCGCAGAGGA 2436
Qy 751 nSerAsnLeuThrIleYs-----AspArgSerMetArgIleYserPheAspMetGlyGly 769
Db 2437 CACCCCGGCTGACAGGCCCGCCGAGGGAACTCGCGGACAGC-----GA 2481
Qy 769 uThrIleuLeuSerValCysProMetValProIleAspLeuGlyIleYsSerIleuValG 789
Db 2482 CACGTCATCTCATCTCCGTCGTCGAGCAGGAGCTGAGAGCTTCTTACCGCGCTT 2541
Qy 789 nAsnLeuIleArgSerThrGluIleuAsnIleGlnIleuSerGlySerGlnSerG 809
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Qy 809 YserArgIleYserGlnAspPheIleYrProIleYrIleArgIleYsLeuPheIleThrAs 829
Db 2602 GCCTTGTGCCAAAGTACAGCCCTTACATTGCGGAGGAGAGCTAGAC-----ACCA 2652
Qy 829 pGluGluVal-----GlyPro-----GluGluThrG 838
Db 2653 CTCCGACCTGTGATCCCGCTGCGGGCCCGGACGAGCTCGGACCGGAGGCTCCCTT 2712
Qy 838 uThrAspThrPheAspAlaIleProGlnProAlaArgGluAlaIlePheAlaSerAsp 858
Db 2713 TGGTACGCGGCTGGGCGCGGCGCGGCGGAGAGTGAAGCGGCGCTGGGC----- 2764
Qy 858 IleuArgThrGlyArgSerArgSerSerGlnSerIleCysIleValAlaGly 874
Db 2765 ---CAGTGACCGCGCGCGGCGCTTCTCAGCAGCGTGTCTCCAGGT 2809

RESULT 8
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCON POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCES: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1

QY	337	AsnLeuIegIncySValTPrpAysSerThpAlaIAsp-----	349
Db	1012	GGTGTGATCCAGTCTGCTGGAGATCTTAAGTACTAACTCTTACAGCAGCAGCTGCAC	1071
QY	350	-----GlnLysSerValSerIleAlaThrTPrpLys-----ProHis	361
Db	1072	TCCACGTGGCAGTACTAGAGCGGACACTACTGCCCCATGTACAGACTATCCACCT	1133
QY	362	LeuLysAlaLeuHisThrCys-----	368
Db	1132	CTGAACCACTGGAGCTGCTGAGAGATCTCAAGCAAAATTCGACTCACTTCAGGAG	1191
QY	369	-----SerProThrAngLInLysSerPheLysGluValArg	382
Db	1192	GAGCCACAGCCAGACCATCAACA---AGTCAGAAAGTCAGTTGTAAGATCGTGTCT--	1245
QY	383	MetalAspProAlaGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp-----	400
Db	1246	TTTCCTACACCCCCAGGAGGTGGTCCCAAGGAAAGGGAGTCTCCCAAGCCCAAGCGCTC	1305
QY	401	ArgArgSerProSerThpAspIleThrAlaGluGlySerProThrLysValGlnLysSer	420
Db	1306	CGCGCGTCCCCAGTCGCGGATCAGAGCTTTATATACACGCCGAGAGAGTCCCAAGGC	1365
QY	421	TPrpSerPheAsnAspArgThpArgPheArgProSerLeuArgLysSerSerGlnPro	440
Db	1366	TGGAGCTTTGGTGAACCGACGCCGACACGCGACTTCCCATCAAGAGGCTGCATCC	1425
QY	441	LysProValIleAlaPAlaAspThrAlaLeuGlnThrAspAspValTyrAspGlnLysGly	460
Db	1426	CGGACGAATTAGAACGAAAGCTCTCT--GGGAGGACATCTGTAAGACACACAGAGC	1482
QY	461	CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla	480
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QY	481	IleArgIleMetLysPheHisValAlaAlaValArgLysPheLysGluThrLeuArgProTyr	500
Db	1543	GTGTGTGTTAAGCGGTTCTTGCTATCTAAGGAAAGTTCAAGAGAGCTTCGCGCCATAT	1602
QY	501	AspValLysAspValIleGluGlnTyrSerAlaGlnHisLeuAspMetLeuCysArgIle	520
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QY	521	LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys	540
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QY	561	ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu	580
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QY	612	AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys	631
Db	1921	CCCTACACACAGCCAGAGAGACGCGTAC-----CATGCAGACAAACATGGCGGT	1971
QY	632	-----LeuSerArgSerThpSerAlaAsnIleSerArgGlyLeuGlnPheIleLeu	648
Db	1972	ATCATTAAGATCGTCCGCTCCACCAAGCTCT-----	2001
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Db      2002 -----ACGGGCTAAGAGACTACGACAGCACCCTCCAGCATC-----CCC 2040
Oy      669 AlaThrgInValProIleSerGlnSer 677
Db      2041 CCTGCCAGATGTCTCTCCTCCCTCCACCTCG 2067

RESULT 10
US-09-177-650-1
/ Sequence 1, Application US/09177650
/ Patent No. 6413719
/ GENERAL INFORMATION:
/ APPLICANT: Leppert, Mark F.
/ APPLICANT: Singh, Nanda
/ APPLICANT: Charlier, Carole
/ TITLE OF INVENTION: KENQ2 AND KENQ3 - POTASSIUM CHANNEL GENES WHICH ARE
/ TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
/ FILE REFERENCE: 2323-134
/ CURRENT APPLICATION NUMBER: US/09/177,650
/ CURRENT FILING DATE: 1998-10-23
/ EARLIER APPLICATION NUMBER: 60/063,147
/ EARLIER FILING DATE: 1997-10-24
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3232
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (128)..(2743)
/ FEATURE:
/ NAME/KEY: mutation
/ LOCATION: (975)..(976)
/ OTHER INFORMATION: There is an insertion of a GT between nucleotides
/ OTHER INFORMATION: 975 and 976 in kindred K1504.
/ FEATURE:
/ NAME/KEY: mutation
/ LOCATION: (978)
/ OTHER INFORMATION: The mutation A to G occurs at this base in kindred
/ OTHER INFORMATION: K3904.
/ FEATURE:
/ NAME/KEY: mutation
/ LOCATION: (1043)
/ OTHER INFORMATION: The mutation G to A occurs at this base in kindred
/ OTHER INFORMATION: K1705.
/ FEATURE:
/ NAME/KEY: mutation
/ LOCATION: (1691)..(1703)
/ OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
/ OTHER INFORMATION: deleted in kindred K3369.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (1039)
/ OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
/ OTHER INFORMATION: the control population.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (1846)
/ OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
/ OTHER INFORMATION: the control population.
/ FEATURE:
/ NAME/KEY: mutation
/ LOCATION: (1469)
/ OTHER INFORMATION: The mutation C to T occurs at this base in kindred
/ OTHER INFORMATION: K1525.
/ FEATURE:
/ NAME/KEY: mutation
/ LOCATION: (1094)
/ OTHER INFORMATION: The mutation C to T occurs at this base in kindred
/ OTHER INFORMATION: K4445.
/ FEATURE:

```

NAME/KEY: mutation
LOCATION: (1125)
OTHER INFORMATION: The mutation G to A occurs at this base in kindred
OTHER INFORMATION: K4516.
FEATURE:
NAME/KEY: mutation
LOCATION: (2736)..
OTHER INFORMATION: There is an insertion of GGCC between these two
US-09-177-650-1

Alignment Scores:

Pred. No.:	2,75e-179	Length:	3232
Score:	1788.00	Matches:	411
Percent Similarity:	58.78%	Conservative:	101
Best Local Similarity:	47.19%	Mismatches:	183
Query Match:	39.32%	Indels:	177
DB:	3	Gaps:	22

US-09-810-796-5 (1-888) x US-09-177-650-1 (1-3232)

QY 17 AlaAlaArgGlyAspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGly 36
DB 227 TCACCCGGAGCGGGCGCTGATCGCCGCTCCAGGCCCAAG-----CGC 277
QY 37 GlyGlyGlyLeuArgGlySerArgGlyGlyGlyAlaArgMetSerLeuLeuGly 56
DB 278 GCGAGCATCTCAAGCAACCTCGCGGGCGCGCGCGCC-----GGG 322
QY 57 LysProLeuSerThrSerSerGlnSerCysArgArgAlaValLysThrArgVal 76
DB 323 AAGCCC-----CCCAAGCGCAAGCCCTTCAACGCAAGCTG 358
QY 77 GlnAsnThrLeuThrAsnValLeuGluArgProArgGlyThrAlaAlaThrLeu 96
DB 359 CAGAAATTCCTTCAACGCTGAGCGCGCGCGCGCTGCTCATCAACGCGC 418
QY 97 PheValPheLeuLeuValPheGlyCysLeuLeuSerValPheSerThrLeuProGlu 116
DB 419 TACGTTCTCTCGTCTTTCTCTGCTGCTGCTGCTGCTTTCCACCAACAGAG 478
QY 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMetLeuValPhe 136
DB 479 TATGAGAAGAGCTCGAGGGGGCGCTCTACATCTGGAATCGTGAATCGTGTTT 538
QY 137 GlyLeuGluPheLeuLeuArgGlyLeuPheSerAlaGlyCysCysArgGlyThrArgGly 156
DB 539 GGGGTGAGTACTTCGTGCGGATCTGGCGCGAGCTGCTGCGCGTACCTGCTCG 598
QY 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 176
DB 599 AGGGGGCGGCTCAAGTTCTTCCCGAAGACGTTCTGTGTATGACATCATGTCTCATC 658
QY 177 AlaSerIleAlaValIleSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
DB 659 GCTTCATTGCGGTGCGCGCGCGCGCTCCAGGGCAAGCTTTGACATCTGGGCTC 718
QY 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThr 216
DB 719 CGAGAGCTGCGCTTCTGAGATTCGCGATATCGCATGAGCCGGGGAGGACCC 778
QY 217 TrpLysLeuLeuGlySerValValIleAlaHisSerIleGluLeuLeuThrAlaTrp 236
DB 779 TGGAGCTGCTGGGCTCTGTGCTTATGCCCAAGCAAGAGCTGTGCTGCTGTAC 838
QY 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValIleLeuValGluLysAspAla 256
DB 839 ATCGGCTTCTTGTCTCATCTGCGCTGCTTCTGCTGCTTGGCAAGAGGGGAG 898
QY 257 AsnLysGluPheSerThrThrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThr 276
DB 899 AAGGACCACTTGTACACTAAGGAGATGACTCTGTGGGGCGCTGTATCAAGCTGACACC 958

QY 277 IleGlyThrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
DB 959 ATTTGGTACGGGAGCAAGTACCACCCAGACTGTGAACGGGAGCTCTTGGCAACCTTC 1018
QY 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
DB 1019 ACCCTCATGTGATCTCTCTTCTTCTGCGCTGCGCATCTTGGGGCTTGGGTTTGGC 1078
QY 317 LeuLysValGlnGlnGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAla 336
DB 1079 CTGAAGTTCAAGAGCAAGCAAGAGCACTTGAAGAGAGGCGAACCAGGAGCA 1138
QY 337 AsnLeuIleGlnCysValTrpArgSerThrAlaAsp----- 349
DB 1139 GGCCTGATCATGTCGGCTGAGATTTCTACGCCCAACCTCTCGGCAACAGCTGCAC 1198
QY 350 -----GlyLysSerValSerIleAlaThrTrpLys----- 359
DB 1199 TCACGTGCGAGTACTACAGAGCAAGCTCACCGCTCCATGTACGTTCCGAACCTCAA 1258
QY 360 -----ProHisLeuValAlaLeuHisThr----- 367
DB 1259 ACCCTACGGGGCTCCAGACTTTTCCCTCCCTGAACCACTGAGCTGCTGAGAACTTC 1318
QY 367 ----- 367
DB 1319 AAGAGTAATCTGACTGCTTTCAGAAAGCAACCCCGCGGAGCGCTTCCAACTAA 1378
QY 368 -----CysSerPro-----ThrAsnGlnLysLeu 375
DB 1379 GCGAGCCGTGAGAGGGCCCTGTGTGATGCTGCGCCGAGCGCTGTGACCAAGAGTTC 1438
QY 376 SerPheLysGluArgValAlaArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 395
DB 1439 AGTTGAAAGATCGTGC--TTCTCAGCCCGGAGGCTGAGCTGCCAAGGAGAAAGGGG 1495
QY 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrIleGluLysSer 413
DB 1496 TCCCGCAGAGCCCAAGCTGTAGGGCGGTCCACCAAGCGGCAAGAGCTCGAGCAAGC 1555
QY 414 ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu 433
DB 1556 CCAGAGAGGTGCCCAAGAGCTGAGCTTGGGAGCCGAGCGGAGCGGACGAGCTTTC 1615
QY 434 ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp 453
DB 1616 CGCATCAAGGGTCCGCGCTCAGCGAGAACTGAA--GAGCAAGCTTCCCGGAGAG 1672
QY 454 AspValIleAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProPro 473
DB 1673 GACATTGTGAGTACAGAGAGCTGCCCTCGAGTTTGTACCGAGAGCTGACCCCGGCG 1732
QY 474 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493
DB 1733 CTCAAAGTCAGCATGAGAGCGCTGTGTCTCATGCGGTTCTGTGTCTCAAGCGAAGTTTC 1792
QY 494 LysGluThrLeuArgProThrAspValLysAspValIleGlnGlnLysSerAlaGlyHis 513
DB 1793 AAGGAGAGCTCGCGCTTCAACAGTATGAGACGTATGAGACAGTACAGCGGCGCAC 1852
QY 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 533
DB 1853 CTGACATCTCTTCCGAAATTAAAGCTGCGCATGCAAGTGGAGCCAGATCGTGGGCGG 1912
QY 534 GlyGlnIleThrSerAspLysSerArgGlyLysIleThrAlaGlnHisGluThrThr 553
DB 1913 GGCACAGCATACAGGAC--AAGGACCGCACCAAGGCGCGCGGAGGAGCTGCCCC 1969
QY 554 AspAspLysSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGlu 573
DB 1970 GAGAGCCCAAGCATATGAGAGCGCTCGGAGAGTGAAGAACAGAGTCTTGTCCATGAGG 2029
QY 574 SerLysLeuAspCysLeuLeuAspIleThrGlnGlnValLeuArgLysGlySerAlaSer 593

QY 82 AsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
::: |||||
Db 283 GAGCGCTTGAGAGACCGCGGGCTGGCGCTTTCACCGCGTTGATTCCTGATT 342
QY 102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrIleLeuAla 121
||| |||||
Db 343 GTCTCGGGGTGCTGATTCCTGCTGCTGACACATTCAGAGAGATAGAGATGCTCTCG 402
QY 122 SerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPheIle 141
||| |||||
Db 403 GGAAGACTGGCTTCTGTACTGAGAGACATTTGCTATTTTCATCTTTGAGACCGAGTTTGGT 462
QY 142 IleArgIleTyrPheSerAlaGlyCysCysArgTyrArgGlyTyrTrpGlnIleArgLeuArg 161
||| |||||
Db 463 TTGAGAGATCTGGGCTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
QY 162 PheAlaArgIleProPheCysValIleAspThrIleValLeuIleLeuIleAlaVal 181
||| |||||
Db 523 TTGACGAGAGAGCGCTGTGACATGTTGACATCTTTGTCTGATTCCTGTGCTGCTGCTG 582
QY 182 ValSerAlaIleTyrGlnIleAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
||| |||||
Db 583 GTTGCCTGGAGAACCAAGCAATGTTCTGGCCACTCC---CTGGAGACCTGGCGCTTC 639
QY 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyIleTyrTrpIleLeuGlnIle 221
||| |||||
Db 640 CTGCAAGATCTGCGCATGCTGCGATGACCGGAGAGTGGCACTGGCAAGCTTCTGGCGC 699
QY 222 SerValValTyrAlaHisSerIleGluIleValIleThrTyrIleGlyPheLeuVal 241
||| |||||
Db 700 TCAGCCATCTGTGCCACAGCAAAAGATCATACGCGCTGGTACATCGCTTCTGACCA 759
QY 242 LeuIlePheSerSerPheLeuValTyrLeuValGluIleAspAla----- 256
||| |||||
Db 760 CTCATCTCTTCTCATTTCTGTCTACCTGCTTGAGAAAGACGTCCACAGAGGTGATGCA 819
QY 257 -----AsnIleGluPheSerThrTyrAlaAspAlaLeuTyrTrpGlyThr 271
||| |||||
Db 820 CAAGAGAGAGATGAAAGAGGTTTGAGACCTATGACAGATGCTGCTGTGGTGGCGCTG 879
QY 272 IleThrLeuThrThrIleGlyTyrGlyAspIleThrProLeuThrThrIleGluIleArgLeu 291
||| |||||
Db 880 ATCAACCTGGCCACCTGCTGATGAGACACCAACCAACCGTGGAGAGCGCTCTG 939
QY 292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeu 311
||| |||||
Db 940 ATTGGCGGCACCTTTTCTTAATTGGCGTCTCTTTTGGCTTCCAGCGGCATCTCG 999
QY 312 GlySerGlyPheAlaLeuIleValGlnIleGlnHisArgGlnIleHisPheGluIleArg 331
||| |||||
Db 1000 GGGTCGGGCTGGCCCTCAAGGTGCGAGCAACCGTCAAGAGCACTTTGAGAAAG 1059
QY 332 ArgAsnProAlaAlaAsnIleGlnIleCysValIleTyrArgSerTyrAlaIleAspGluIle 351
||| |||||
Db 1060 AGAAGCCAGCTGCTGATCTGAGCTCAGGCTGCTGAGGATTAATTAACCAACCCCAAC 1119
QY 352 SerValSer---IleAlaThrTyrIle-----ProHisLeu 362
||| |||||
Db 1120 AGGATTGACCTGGTGGCACTGAGATTTTATGATCACTGCTCTTTCTTTCTTCTTC 1179
QY 362 LysAlaIleLeuHisThrCysSerProThrAsnGlnIleLeuSerPheIleGluIleArg 382
||| |||||
Db 1180 AGCAAAAGAACAGCTGAGCAGATCCAGCCAAAGCTGGCTTCTTGGATCGGGTTCC 1239
QY 383 MetAlaSerProArgIleGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIle 402
||| |||||
Db 1240 CTTTCTTAATCTCTGAGTGAACATACTAA-----GGAAGCTATT 1281
QY 403 SerProSerThrAspIleThrAlaGlnIleGlySerProThrIleValGlnIleSerIleTyr 422
||| |||||
Db 1282 ACCCGCTGTAATGATGATGCACTAGAAAGAAAGTCTTCTTAAGAACCAAGCGCTTGGC 1341
QY 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuIle----- 436

Db 1342 TTAACAATAAAGACGTTTCGCGACGGCTTCCCGCATGAAGCTTACGCTTTCTGGCAG 1401
QY 437 SerSerGlnProIleProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr 456
||| |||||
Db 1402 AGTTCTGAA-----GATCCCGGACAGCT-----GACCCCATGGCG 1437
QY 457 AspGluIleGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuIleThr 476
||| |||||
Db 1438 GAAAGCAGGGGCTATGGAAATGATCTCCCATCGAAGACATGATCCACCTGAAGGCC 1497
QY 477 ValIleArgAlaIleArgIleMetIlePheHisValAlaIleArgIlePheIleGluIleThr 496
||| |||||
Db 1498 GCCATCCAGCGCTGAGATTCATCAATTCGCTCTTAATAAAAAATTCAAGAGAGACT 1557
QY 497 LeuArgProIleArgValIleAspValIleGlnIleTyrSerAlaGlyHisLeuAspMet 516
||| |||||
Db 1558 TTGAGGCTTACGATGATGAAGATGTGATGTGAGCATTTCTGCGCGGCATCTCCACATG 1617
QY 517 LeuCysArgIleIleSerLeuGlnThrArgValaAspGlnIleLeuGlyIleGlnIle 536
||| |||||
Db 1618 CTTTCCAGATTAAGTATACCTTCAGACGAAATATGATTTTCAACCCCTGACCTCC 1677
QY 537 ThrSerAspIleIleSerArg----- 543
||| |||||
Db 544 -----GluIleIleThrAlaGlnIleGluIleThr-----AspAspLeuSer 557
||| |||||
Db 1738 TCTCCAGAGATGAACCATATGTAGCCAGACCATCACTCACTGAAGATGAAGACCAAGC 1797
QY 558 MetLeuGlyArgValValIleValGluIleValGlnIleGlnIleGlnIleGlnIleGlnIle 577
||| |||||
Db 1798 ATGATGGGGAAGTTGTAAAGTTGAAGACAGGTTTCAAGACATGGGGAAGACCTGGAC 1857
QY 578 CysLeuLeuAspIleTyrGlnIleValLeuArg----- 588
||| |||||
Db 1858 TTCTCGGATATGACATGACATCAACATGAAACGTTGACAGTCCAGGTACGAGATAT 1917
QY 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPhe 605
||| |||||
Db 1918 TACCCACCAAGGACCTCTCG-----CCAGCT 1947
QY 606 GluIleGlnIleThrSerAspTyrGlnIleSerProValaAspSerIleAspLeuSerGlySer 625
||| |||||
Db 1948 GAAAGAGAGAGAGAGAGAGAGAGATTC---GATTGGAATAACATCATCTGCAAC 2004
QY 626 AlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgIleGln 645
||| |||||
Db 2005 TATTTGAGACAGGCCCCCGGAACCACTACAGCTTCCAC----- 2046
QY 646 PheIleLeuThrProAsnGluPheSerAlaGlnThrPheIleValLeuSerProThrMet 665
||| |||||
Db 2047 ---CAGGTGACCATTTGACAAAGTCAAGCCCTATGGGTTTTTGGCATGACCT----- 2097
QY 666 HisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIleThr 685
||| |||||
Db 2098 -----GTGAACCTGCCCCGAGGGAGACCAGTTCTGAAAGTTTCAGGCAACT 2145
QY 686 AsnThrIleAlaAsnGlnIleAsnThrAlaProIleProAlaIleProThrIleGln 705
||| |||||
Db 2146 -----CTCTCTTCTCAAGCAACAGTATGGAG 2175
QY 706 IleProProProLeuProAlaIleIleHisIleProArgProGluThrIleHisProAsn 725
||| |||||
Db 2176 AGGCCAGAGTCTGCTATCTGACTCTTCTCACTCCCAAGTACGCTGCCA---TCC 2232
QY 726 ProAlaGlyLeuGlnIleGlnIleSerAspValThrThrCysLeuValAlaSerIleGlu 745
||| |||||
Db 2233 CAGGTGACCTGACAGGCCCCCTACTCGAC----- 2262
QY 746 AsnValGlnValAlaGlnSerAsnLeuThrIleAspArgSerMetArgIleSerPheAsp 765
||| |||||

Db 2263 CGATCTCCCCCGGAG-----AGACGTAGCATCAG 2295
Qy 766 MeGlyglunthrlleuSerValCysPrometValProlysAspLeuGlyLysSer 785
Db 2296 CGAGACGATACACACTCTGCTCTG----- 2222
Qy 786 LeuSerValGlnleuLeuLeuIleArgSerThrGlnGlnleuAsnIleGlnLeuSerGlySer 805
Db 2323 ATGCGGTCAACGC-----GAGAGCTGAGAGAGCTCTCCAAAGTGGCTTC 2367
Qy 806 GluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTTPArg 821
Db 2368 AGCATCTCCGAGACAGATGATGATTATGTGTGCGCCCAATGGGGGTGAGCTGGATG 2427
Qy 822 GluSerLysleuPheIleThrAspGlnGluValGlyProGlnGlnthrlGlnthrlAspThr 841
Db 2428 AGGAGAGAGCGGATCTCGCCGAG-----GGTAGAGGAGACAGACAGACGAGCC 2478
Qy 842 Phe 842
Db 2479 TTC 2481
RESULT 13
US-09-177-650-6
Sequence 6, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BNFC)
TITLE OF INVENTION: AND OTHER EPILEPTSES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2914
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(2634)
FEATURE:
NAME/KEY: allele
LOCATION: (840)
OTHER INFORMATION: The polymorphism of a T to a C at this position
OTHER INFORMATION: has appeared in one individual.
FEATURE:
NAME/KEY: mutation
LOCATION: (947)
OTHER INFORMATION: The missense mutation from a G to a T occurs at
OTHER INFORMATION: this position in a BNFC family.
FEATURE:
NAME/KEY: allele
LOCATION: (678)
OTHER INFORMATION: This position is polymorphic for C or T.
FEATURE:
NAME/KEY: allele
LOCATION: (750)
OTHER INFORMATION: This position is polymorphic for T or C.
FEATURE:
NAME/KEY: allele
LOCATION: (1089)
OTHER INFORMATION: This position is polymorphic for G or C.
FEATURE:
NAME/KEY: allele
LOCATION: (2598)
OTHER INFORMATION: This position is polymorphic for T or C.

US-09-177-650-6
Alignment Scores:
Pred. No.: 5,37e-158 Length: 2914
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
DB: 3 Gaps: 28
US-09-810-796-5 (1-888) x US-09-177-650-6 (1-2914)
Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaIleArgLysArgLys 22
Db 163 GAGGTGAGCA-----GTCACTTGCGCCTCGGGGCCGAGCCGACCAAGACGG 213
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
Db 214 ACCCTGCTCTG-----GAGGGCGGGCGCGGAGAGGG 249
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 250 CAGCGAGAGACCCCGAGGAGC-----ATCGGGCTCTGACCAAGACCCCGTGAAGCCG 303
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 304 CCAGTCAAG-----AGAAACAAAGCCCAAGTACCGGCGCATCCAACTTGATCTAC 354
Qy 82 AsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
Db 355 GAGCGCTGAGAGACCGCGGGCTGGCGCTTACACAGCGCTTGATGATCTGAT 414
Qy 102 ValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlnHisThrLysLeuAla 121
Db 415 GTCTCGGGGTCTGATCTGCTGCTGCTGACCACTTCAAGAGATAGACTGTCTG 474
Qy 122 SerSerCysLeuLeuLeuGlnPheValMetIleValPheGlyLeuGlnPheIle 141
Db 475 GAGACTGCTTCTGTTACTGAGAGACATTGCTATTTCATCTTTGAGCCGAGTTGCT 554
Qy 142 IleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrPngIlyArgLeuArg 161
Db 535 TTGAGGATCTGGGCTGCTGATGTTGCTGCCGATCAAGAGCTGCGGGCCGACAGAG 594
Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
Db 595 TTGGCCAGAGAGCCCTGTGCATGTTGACATCTTGTGCTGATTGCTGTGCGCAGTG 654
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
Db 655 GTTGTCTGGGAAACCAAGGCAATGTTCTGGCCACTCC---CTGGAAAGCTGGCGCTTC 711
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyIlyThrTrpLysLeuLeuGly 221
Db 712 CTGCAATCTCTGGGATGCTGCGGATGACCGGAGGTGTCACCTGGAAGCTTCTGGGC 771
Qy 222 SerValValTyrAlaHisSerLysGlnLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241
Db 772 TCAGGCATCTGTGCCACAGCAAAAGATCATTCACGGCTGTGATCGGTTCTCCAGCA 831
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGlnLysAspAlaLeuTrpTrpGlyThr 256
Db 832 CTGATCTTCTTCTCATTTCTGTCTACCTGTTGAGAAAGACGTCCTCAGAGTGATGA 891
Qy 257 -----AsnLysGlnPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThr 271
Db 892 CAAGAGAGAGATGAAGAGAGATTGAGACCTATGACAGATGCCCTGTGGTGGGCTTG 951
Qy 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeu 291
Db 952 ATCACACTGGCCCACTTGTGCTATGAGACCAAGACCCCAAAACGTGGAGGCGCTCTG 1011
Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPheAlaLeuProAlaGlyIleLeu 311

Db 1012 ATTCGCGCACCTTTCTTAATGCGCTCTCTTTTTCGCTTCACGGGCGCATCTCG 1071
Qy 312 GYSErGlyPheAlaLeuIysValGlnGluGlnHISrGlnIlyshIspHegIlyIysrG 331
Db 1072 GGGTCGGGGCTGGCCCTTCAGAGTCGAGACCAACCGTCAGAGCATTTGAGAAAAG 1131
Qy 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAspGlyIys 351
Db 1132 AGGAACCCAGCTGCTGAGCTCATTCAGGCTGCTGAGGATATTGCTACCAACCCCAAC 1191
Qy 352 SerValSer---IleAlaThrTrrIys-----ProHisIleu 362
Db 1192 AGGATTGACCTGGCGACATGAGAGATTTTATGAATCAGTCCTCTTTTCTTTCTTC 1251
Qy 363 IysAlaLeuHISrCysSerProThrAsnGlnIlyLeuSerPheIysGluArgValArg 382
Db 1252 AGGAAGAAACAGCTGAGGACGATCCAGCAAAAGCTGGCTCTTGGATCGGGTTCCG 1311
Qy 383 MetAlaSerProArgGlyGlnSerIleIysSerArgGlnAlaSerValGlyAspArg 402
Db 1312 CTTCCTAATCTCTGCTGAGCAATACTAAA-----GGAAAGCTATTT 1353
Qy 403 SerProSerThrAspIleThrAlaGluGlySerProThrIlyValGlnIlySerTrrPser 422
Db 1354 ACCCTCTGAATGTAGATGCCATAGAAAGAGCTCTTAAAGAACCAAAAGCTGTGGC 1413
Qy 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuIys----- 436
Db 1414 TTAACAATTAAGAGGCTTCCGACGGCTTCGGATGAAGACCTACCGCTTCTGGCAG 1473
Qy 437 SerSerGlnProIysProValIleAspAlaAspThrAlaIleuGlyThrAspAspValTyr 456
Db 1474 AGTTCTGAA-----GATGCCGGACACAGT-----GACCCCAATGGC 1509
Qy 457 AspGlnIlyGlyCysGlnCysAspValSerValGluAspLeuThrProIleuIysThr 476
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Qy 537 ThrSerAspIlyIysSerArg----- 543
Db 1750 TCCAGCCCAAACACAAAGAGTCCGAAGAGGTCAGATTCACTTCCATCCCAAGAA 1809
Qy 544 -----GluIysIleThrAlaGluHISrGluThrThr-----AspAspLeuSer 557
Db 1810 TCTCCAGAGATGAAACCATATGTATGTAGCCAGACCATCCACAAATTCAGAGCCAAAG 1869
Qy 558 MetLeuGlyArgValIlyValIysValGlyIysGlnValGlnSerIleGluSerIysLeuAsp 577
Db 1870 ATGATGGGGAAGTTTGTAAAGTTGAAGACAGTTTCAGACATGGGGAAAGAGCTGAGC 1929
Qy 578 CysLeuLeuAspIleTyrGlnGlnValIleuArg----- 588
Db 1930 TTCTCTGTGATATGCATGCACAAACATGAAGAGGTTGCAAGTGCAGGTCACGAGTAT 1989
Qy 589 -----LysGlySerAlaSerAlaIleuAlaIleuAlaSerPheGlnIleProPhe 605
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Qy 646 PheIleIleuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMet 665
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Qy 666 HisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIleThr 685
Db 2170 -----GTAACTGCTCCCGAGGGGAGACCCAGTTCTCGAAAGGTTGAGCAACT 2217
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Parent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177, 650
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 2814
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:

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; LOCATION: (202)...(2811)
US-09-177-650-90

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US-09-810-796-5 (1-888) x US-09-177-650-90 (1-2814)

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QY 102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121
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QY 122 SerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPheIle 141
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DB 772 TTTCAGAGAAAGCCCTGTCATGTGAGCATCTTGACTGATTGCTGTGCGCAGTG 831
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QY 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrPGLYThr 271
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QY 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrLeuGlyArgLeu 291
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Search completed: October 23, 2005, 19:18:31
Job time : 340 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: October 23, 2005, 18:01:06 ; Search time 1087 Seconds

(without alignments)
6738.945 Million cell updates/sec

Title: US-09-810-796-5

Sequence: 1 MKDVEGSRGVLLNSAARG.....SICKAGESTDALSLPHVKLK 888

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Searched: 9772231 segs, 4124568258 residues

Total number of hits satisfying chosen parameters: 19544462

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4547	100.0	2772	9 US-09-825-147-1	Sequence 1, Appli
3	4547	100.0	2772	19 US-10-803-268-1	Sequence 1, Appli
4	4547	100.0	3111	9 US-09-825-147-3	Sequence 3, Appli
5	4547	100.0	3111	9 US-10-803-268-3	Sequence 3, Appli
6	4527.5	99.6	2694	9 US-09-866-020-1	Sequence 1, Appli
7	4527.5	99.6	2694	9 US-09-810-796-2	Sequence 2, Appli
8	4527.5	99.6	2694	21 US-10-948-483-1	Sequence 1, Appli
9	4527.5	99.6	3137	19 US-10-661-623-1	Sequence 1, Appli
10	4523.5	99.5	3071	9 US-09-810-796-1	Sequence 1, Appli
11	4513.5	99.3	3074	9 US-09-813-148-1	Sequence 1, Appli
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19	1797	39.5	7407	21 US-10-482-834A-58	Sequence 58, Appli
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45	1604	35.3	1878	20 US-10-744-796-3	Sequence 3, Appli

ALIGNMENTS

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; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; TITLE OF INVENTION: KNOX, A No. US20020102677A1et Pectasium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3

LENGTH: 2667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
NAME/KEY: CDS
LOCATION: (1)..(2667)
OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Alignment Scores:

Pred. No.:	0	Length:	2667
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QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrThrLysLeuLeu 220
DB 601 TTCCTACAGATCTCCGCGATGGTGCATGAGACCGAAGGGAGGACCTTGAATTAATCTG 660
QY 221 GlySerValValTyrAlaHisSerLysGluValIleThrAlaTyrTyrIleLysPheLeu 240
DB 661 GGTTACAGTGTATATGCTCACAGCAAGAAATTAATCACAGTTGTATACATTAAGATTTTGG 720
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 721 GTTCTTATTTTTCGCTTCTTCTGTATCTGTGTGAGAAAGATGCCCAATTAAGAGTTT 780

QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 781 TCTACATATGACAGATGCTCTGTGGGGCACAATTATCATTTGACAACTATTGGCTATGGA 840
QY 281 AspLysThrProLeuThrThrTrpLeuGlyValGlyLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 841 GACAAACCTCCCTCACTTGGCTGGGAAGATTTGCTTTCGACAGGCTTTCGACTCTTGGGC 900
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 901 ATTTCTTCTTTCGACTTTCCTGCGGCAATCTTGGCTCAGGTTTTCATTAAAGTTACAA 960
QY 321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAspProAlaAlaAsnLeuIleGln 340
DB 961 GACACACACCGCCGAGAAACACTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCCTCATTCAG 1020
QY 341 CysValIleTyrArgSerTyrAlaAlaAspGlyLysSerValSerIleAlaThrTyrLysPro 360
DB 1021 TGTGTTTGGCGTATGTTAGCAGCTGATGAGAAATCTGTTCCATTGCAACCTCGAAGGCCA 1080
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
DB 1081 CACTTGAAGGCTTTCACACCTTCAGCCCTTACCAATCGAAAGCTTATTTAAGAGCGCA 1140
QY 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
DB 1141 GTGGCATAGGCTTAGCCCGAGGGGCCAGAGTATTAAGACCCGACCAAGCTCAGTAGTAC 1200
QY 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
DB 1201 AGGAGGTCCCAAGACCAAGACATCAACAGCGGCACTCCACCAAGTGCAGAAAGAGC 1260
QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuAlaGlyLysSerSerGlnPro 440
DB 1261 TGGAGCTTCAACGACCGAACCCTTCGGGCCCTCGCTCGCCCTCAAAAGTTCTTAGCCA 1320
QY 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGlyLysGly 460
DB 1321 AAACCAAGATAGATGCTGACACAGCCCTTGACCTGATGTATATGATGAAAAAGCA 1380
QY 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
DB 1381 TGCCAGTGTGATGATCAAGTGAAGACCTCACCCACCACTTAAACCTGATTCGACCT 1440
QY 481 IleArgIleMetCysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
DB 1441 ATCAGAAATTAAGAAATTTCACTTGCAGAAACGAAAGTTTAAGAAACCTTACGTCCAAAT 1500
QY 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
DB 1501 GATGTAAAGATGATCATTAAGAAATTTCTGCTGTCTGATCTGACATGTTGTGTGAAATTT 1560
QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
DB 1561 AAAAGCTTCAAAACAGGTGATCAAAATTTGTGAAAAAGGCAAAATCACATCAGATCAAG 1620
QY 541 LysSerArgGlyLysIleThrAlaGlnHisGluThrTyrAspAspLeuSerMetLeuGly 560
DB 1621 AAGAGCGAGAAATAACAGCAAGCAATGAGACACAGACGATCTCAGATGCTCGGT 1680
QY 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
DB 1681 CGGGTGTGCAAGTTGAAAAACAGTACAGTCCATAGGTCCAAAGCTGGAATGCTTACTTA 1740
QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaSerPhe 600
DB 1741 GACATCTATCAACAGGTCTTCGAAAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTC 1800
QY 601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
DB 1801 CAGATCCCACTTTTGAATGTGAACAGACATCTACATCAAAAGCCCTGTGTGATGACAA 1860
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640

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Db GATCTTCCGGGTTCCGCAAAACAGTGGCTTATCCAGATCACTACTGCGCAACATC 1920
Qy SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db TCAGAGAGCGCTGAGTTCACTTGAAGCCAAATGAGTCACTGTCGCCAGACTTCTACGGC 1980
Qy LeuSerProThrMechHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db CTTAGCCCTACTATGACAGTCAAGCAACAGGTGCCAATTAGTCAAGCGATGGCTCA 2040
Qy AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProIlyProAlaAla 700
Db GCAGTGGACAGCCACCAACCACTTGCACCAATAAATACGCGACCCAGACCGACGAGCC 2100
Qy ProThrThrLeuGlnIleProProProLeuProAlaIleIlyshiSleuProAlaProGlu 720
Db CCAACAACTTTACAGATCCCACTCTCCAGCCATCAAGATCTGCCAGCGCCAGAA 2160
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Qy ValAlaSerIlySerGluAsnValGlnValAlaGlnSerAsnLeuThrIlyAspArgSerMet 760
Db GTTGCCCTCCAGAGAAATGTTCAAGTTGACAGTCAAACTCAACCAAGACGTTCTATG 2280
Qy ArgIlySerPheAsnMetGlyGlyGluThrLeuLeuSerValCysProMetValProIly 780
Db AGAAAAAGCTTTTACATGGAGAGAGAAACCTCTGTCTGTCTGTCTCCATGATGGCGAAG 2340
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Db GACTTGGGCAAACTTTGTCTGTGCGCAAACTGATCAGTCCGACCGAGAACTGAAATTA 2400
Qy GlnLeuSerGlySerGlySerGlySerArgGlySerGlnAspPheTyrProIlyTyr 820
Db CACTTTCAAGAGAGTGAAGTCAAGTGGCTCCAGAGCGACCAAGATTTTATCCCAATGG 2460
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Db AGGAAATCCAAATGTTTATTAAGTGAAGAGTGGTCCCGAAGAGACAGAGACAGAC 2520
Qy ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db ACTTTTGAATGCCGACCGCAGCTGCCAGGAAAGCTGCTTTCATCAGACTCTTAAGG 2580
Qy ThrIlyArgSerArgSerSerGlnSerIleCysLeuValAlaGlyLeuSerThrAspAlaLeu 880
Db ACTGAAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAAGAAAGTACAGATGCCCTC 2640
Qy SerLeuProHisValIlySleuIly 888
Db AGCTTGCCCTCATGTCAAACTGAAA 2664
RESULT 2
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mehle, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255

;; PRIOR FILING DATE: 2000-04-03
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 2772
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-09-825-147-1
Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)
Qy 1 MetLysAspValAlaGlySerGlyArgValAlaLeuAsnSerAlaAlaArgGly 20
Db 106 ATGAAGAGATGAGTGGAGTCGGGCGGAGAGTGTCTGAATCTGGCAGCCCGCAGGGC 165
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyLeu 40
Db 166 GACGGCTGCTACTGCTGGGACCCGCGCGCACGCTCGATGCGCGCGGCGGCTG 225
Qy 41 ArgGluSerArgArgIlyIlySerGlnGlyAlaArgMetSerLeuLeuGlyIlyPheLeuSer 60
Db 226 AGGAGAGCGCGCGGCGGAGAGAGGCGCGGATGAGCTCTGCGGAAAGCCGCTCT 285
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValIlyTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTACGCCAGAGCTGCCGCGCAACCTCAAGTACCGCGGTCAGAACTACCTG 345
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACAAGCTCTGAGAGAGACCCGCGGCTGGGCTTCATCTACACGCTTTCGTTTTCTC 405
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrIlyLeu 120
Db 406 CTTGCTTTGGTGTCTGATTTTGTCAAGTGTTCACCATCCCTGAGACACAAATTTG 465
Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValIlePheGlyLeuGluPhe 140
Db 466 GCCTCAAGTTGCTCTTGAATCTTGAAGTTCGATGATTTGTCTTGGTTGGAAGTTC 525
Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnIlyArgLeu 160
Db 526 ATCATTGCAATCTGGTCTGCGGTTGCTGTGTGATATAGAGATGCAAGAAAGACTG 585
Qy 161 ArgPheAlaArgIlyPheProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 586 AGGTTTGCAGAAAGCCCTTGTGTATATAGTATACCATTTCTTATCGCTTCATATAGA 645
Qy 181 ValValSerAlaIlyThrGlnIlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 646 GTTGTTCGCAAAAACCTAGAGGTATATTTTTCACAGTCTGCACCTCGAAGTCTCGGT 705
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgIlyIlyThrTyrIlyLeuLeu 220
Db 706 TTCCTACAGATCTCGCATGTGTGCGCATGACCGAAGGAGGACACTTGAATTAATCTG 765
Qy 221 GlySerValValTyrAlaHisSerIlyGluLeuIleThrAlaIleTyrTyrIleGlyPheLeu 240
Db 766 GGTTCAGTGTATATGCTCACAGCAAGAAATTAATCACAGCTGTGATCATAGAAATTTTG 825
Qy 241 ValIleIlePheSerSerPheLeuValTyrLeuValGluIlyAspAlaAsnIlyGluPhe 260
Db 826 GTTCTTATTTTTCGCTTCTTCTGTCTATCTGGTGAAGAAAGATGCCAATAAAGATTT 885
Qy 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280

Db 886 TCTACATATGACAGATGCTCTGTGGGGGACAAATTACATTGACAACTATTGGCTATGGA 945
Qy 281 AaplyeThrProleuThrTrpleuGlyArgleuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 946 GACAAAACCTCCCTAACTTGGCTGGGAAGATTCTTTCGACAGCTTTTGCACTTCCTGGC 1005
Qy 301 lIeSerPhePheAlaLeuProAlaGlylIeLeuGlySerGlyPheAlaLeuValGln 320
Db 1006 ATTTCTTCTTTCGACTTCTGCGGCACTTCTGCTCAGGTTTTCATTAAAGATACAA 1065
Qy 321 GluGlnHisArgGlnIlyHisPheGlyLysArgArgAsnProAlaAlaLeuLeuIleGln 340
Db 1066 GAACAACACCGCGAGAAACCTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCATCTCAG 1125
Qy 341 CysValTrpArgSerTyrAlaAlaAspGlyLysSerValSerlIeAlaThrTrpLysPro 360
Db 1126 TGTGTTTGGGCTATGTAACCGACGTGATGAAATCTGTTTCCATTGCCAACCTGGAAAGCA 1185
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGlyArg 380
Db 1186 CACTTGAAAGGCTTGGACACCTGACAGCCCTACCAATCAGAAAGCTAAGTTTAAAGAGCGA 1245
Qy 381 ValArgMetAlaSerProArgGlyGlnSerlIeLysSerArgGlnAlaSerValGlyAsp 400
Db 1246 GTGCGATGAGCTAGCCCGAGGGCCAGAGTATTAAAGACCGAACCTCAGTAGGTGAC 1305
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Db 1426 AAACCGATGATGATCTGACACAGCCCTTGGCAGCTGATGATATATATGAAAAAGAA 1485
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Qy 481 lIeArglIeMetLysPheHisValAlaLysArgLysPheLysGlnThrLeuArgProTyr 500
Db 1546 ATCAGAAATTATGAAATTTTCATGTTGCMAAACGGAATTTAAAGAAACATTAGCTCATAT 1605
Qy 501 AspValLysAspValIleGlnGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1606 GATGTAAAGATGTCATTGAACATATTTCTGCTGATCATCTGGACATGTTGTGTAAT 1665
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1666 AAAAGCCTTCAAAACAGTGTGATCAAAATTTCTGAAAAAGGGCAATTCATCAGATAG 1725
Qy 541 LysSerArgGlyLysIleThrAlaGlyHisGlyLysThrAspAspLeuSerMetLeuGly 560
Db 1726 AAGAGCCGAGAAATAACAGACAACTGAGAACACAGATCTCAGTATGCTCGGT 1785
Qy 561 ArgValValLysValGlyLysGlnValGlnSerlIeGlySerLysLeuAspCysLeuLeu 580
Db 1786 CCGGTGTGTAAGTTGAAAAACAGTACAGTCCATGAAATCCAAAGTGGAGCTCTACTA 1845
Qy 581 AapIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1846 GACATCTATCAACAGAGTCTCTCGAAAGGCTGCTCAGCCCTGCTTGGCTTCATTTC 1905
Qy 601 GlnIleProProPheGlyCysGlyGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1906 CAGATCCCACTTTTAATGTGAACAGACATCGATATCAAAAGCCCTGTGATGACAAA 1965
Qy 621 AapLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaLeuIle 640
Db 1966 GATCTTTCGGGTTCCGACAAACAGTGGCTGCTTATCCAGATCAACTGTCGCAACATC 2025

Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAla 660
Db 2026 TCGAAGAGCCCTGACAGTTCATTCGACGCCAAATGATGATTCAAGTCCCAAGCTTTCTACGG 2085
Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2086 CTTACCCCTACTATGACAGTCAAGCAACACAGGGGCCAAATTAGCAAAAGCGATGGCTCA 2145
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2146 GCAGTGGAGCCACCAACACATTGGCAACCAATTAATAGGACCCAGACGACAGCC 2205
Qy 701 ProThrTrpLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2206 CCAACAACTTAAAGATCCACATCTCTCCAGCCATCAAGATCTGCCAGGCCAGAA 2265
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerlIeSerAspValThrThrCysLeu 740
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Db 2566 AGGGAATCCAAATGTTTATATCATGATGAAGAGTGGCTCCCGAAGACAGAGACACAGC 2625
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RESULT 3
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255

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; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-810-268-1

Alignment Scores:
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Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-810-796-5 (1-888) x US-10-803-268-1 (1-2772)

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Db 226 AGGAGAGCGCGCGGGCGAAGCGGGGCGCGGATGAGCTGCTGGGGAAAGCGCTCTCT 285
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1066 GAACAAACACCGCCAGAAACACTTGGAAAAGAGAACCCAGCTGCGCAACTCATTTAG 1125
QY 341 CysValTyrArgSerTyrAlaAlaAspGlyLysSerValSerIleAlaThrTyrPro 360
Db 1126 TGTGTTGGCGTATGATACGACCTGATGGAATCGTTTCATTTGCAACTGGAAGCCCA 1185
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1186 CACTTGAAGCCTTGACACACTGCAAGCCTTACCAATCAGAACTAATTTAAGAGCGCA 1245
QY 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1246 GTGCGCATGGCTTAGCCCGGCGCCAGAGTATTAAGAGCGCAAGCCCTCAGTAGGTGAC 1305
QY 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1306 AGAGAGTCCCAAGCACCAACATCAAGCGAGGAGTCCCAACCAAACTGCAAGAGAGC 1365
QY 421 TyrSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1366 TGGAGCTTCAAGACCGCAAGCCGCTTCCGCGCTCGCTCGCTCAAAAGTTCTCAGCCA 1425
QY 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1426 AAACCATGATAGAGTCTGACACAGCCCTTGCACTGATGATATATGATAAAAGGA 1485
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1486 TGCAGTGTAGATGATCACTGGAAGACTGACCCCAACCTTAACATCTCATTTGAGCT 1545
QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGlyThrLeuArgProTyr 500
Db 1546 ATCAGAAATTAATGAATTTCACTTGCAAAACGGAAGTTTAAGAAACATTAGCTCATAT 1605
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Db 1606 GATGTAAAAGATGCTATTGAAACAAATATCTGCTGTCATCTGACATGTTGTGTGAATT 1665
QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1666 AAAAGCTTCAAAACAGTGTATGATCAAAATCTTGGAAAAGGCAAAATCACTACAGATAAG 1725
QY 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1726 AAGAGCCGAGAAATAATCAACAGAACTGAGACCAAGAGATCTCATGTGCTCGCT 1785
QY 561 ArgValLysValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1786 CGGTGTGCTCAAGTGTGAATAAAGAGTCAATGATGATCCAAAGCTGAGCCCTACTCA 1845
QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1846 GACATCTATCAACAGGTCTCTGGAAGGCTGTGCTCAGCCCTGCTTGGCTTCATTC 1905
QY 601 GlnIleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1906 CAGATCCCACTTTTGAATGTAAGACATCTGACTATCAAAAGCCGTGTGATGCAAA 1965
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1966 GATCTTTCCGGTTCGCGCAAAACAGTGGCTCTTATCCAGATCAACTAGTCCAAACATC 2025
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QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
| | | | |
Db 2026 TCGAGAGGCGCTGAGTTCATTCGACGCCAAATGATGATTCAGTCCAGACTTTCTACGGG 2085
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
| | | | |
Db 2086 CTTAGCCCTCACTATGACAGTCAAGCACACAGGTGCCCAATTAGTCAAGCGGTGCTCA 2145
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProAspProAlaAla 700
| | | | |
Db 2146 GCAGTGGCAGCCCAACACCATTCGCAACCAATTAATACGACCCCAAGCCAGCAGCC 2205
QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLeuHisIleLeuProArgProGlu 720
| | | | |
Db 2206 CCACAACACTTTACAGATCCCACTCTCTCCAGCATCAAGATCTGCCCGCAGCCAGAA 2265
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740
| | | | |
Db 2266 ACTCTGACCCCTTAACCTCGACGCTTACAGAAAGCATTTCTGACCTCAACCTGCCCTT 2325
QY 741 ValAlaSerIleGlnAsnValGlnValAlaGlnSerAsnLeuThrIleAspArgSerMet 760
| | | | |
Db 2326 GTTGCTCCAGAGAAATGTTCAAGTTGCAAGTCAAAATCTCAACAGAACCGTTCTATG 2385
QY 761 ArgIleSerPheAspMetGlyGlyGlnThrLeuLeuSerValCysProMetValProlys 780
| | | | |
Db 2386 AGGAAAGCTTGACATGGAGAGAAACTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2445
QY 781 AspLeuGlyIleSerLeuSerValGlnAsnLeuIleArgSerThrGlnIleLeuAsnIle 800
| | | | |
Db 2446 GACTTGGGCAAACTTTGTTCTGTGCAAAACCTGATAGGTCAACCAAGAACCTGAATATA 2505
QY 801 GlnLeuSerGlySerIleSerGlySerArgGlySerGlnAspPheTyrProlyStrp 820
| | | | |
Db 2506 CAACCTTCAGGAGATGATCAAGTGCCTCAGAGGACCAAGATTTTACCCTCAATGG 2565
QY 821 ArgGlnSerIleLeuPheIleThrAspGlnGluValGlyProGlnGlnThrGlnThrAsp 840
| | | | |
Db 2566 AGGGAATCCAAATTTGTTTAATGATGAAAGGTGGTCCGAGAGACACAGACAGAC 2625
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGlnAlaAlaPheAlaSerAspSerLeuArg 860
| | | | |
Db 2626 ACTTTGATGCGCACCGGACCTGCGAGGAAAGCTGCTTTGCACTCAACCTCTCAAGG 2685
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysIleAlaGlyIleSerThrAspAlaLeu 880
| | | | |
Db 2686 ACTGGAAAGTCAAGATCATCTCAGAGCATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2745
QY 881 SerLeuProHisValIleLeuLys 888
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Db 2746 AGCTTGCTCATGTCTCAAACTGAAA 2769

RESULT 4
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-3 (1-3111)

QY 1 MetIleAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20
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Db 165 ATGAAGATGTGAGTCCGGCCGGGCGAGGGTGTCTGAACCTCGGCGACCGCCAGGGGC 224
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
| | | | |
Db 225 GAGGCTCTGCTACTGCTGGGACCCGCGGCGCACGCTCGGTGGCGGCGGCTGCTG 284
QY 41 ArgIleSerArgGlyIleGlnGlyAlaArgMetSerLeuGlyIleProLeuSer 60
| | | | |
Db 285 AGGAGAGACCCCGGGGCAACAGGGGGCCCGATGAGCTCTGTGGAGAACCCGCTCT 344
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValIleTyrArgArgValGlnAsnTyrLeu 80
| | | | |
Db 345 TACAGAGATACCCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGTGACAACTACCTG 404
QY 81 TyrAsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
| | | | |
Db 405 TACAACTGCTGAGAGAGACCCCGGCGCTGGCGCTTCACTACACGCTTCTGTTTCTC 464
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrIleLeu 120
| | | | |
Db 465 CTGTGCTTGGTCTGATTTTGTGACGTGTTTCTACCATCCCTGAGCACACAAATTTG 524
QY 121 AlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValIlePheGlyLeuGlnPhe 140
| | | | |
Db 525 GCCCTCAAGTCCCTCTGATTCCTGAGTTCGATGATGTCGTGTTGGAGTTG 584
QY 141 IleIleArgIleTyrPheSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
| | | | |
Db 585 ATCATTCGAATCTGCTGCGGGTTCGCTGTGATTAAGATGAGATGSCAAGAAAGACTG 644
QY 161 ArgPheAlaArgIleProPheCysValIleAspThrIleValIleLeuIleAlaSerIleAla 180
| | | | |
Db 645 AGGTTTGCTGAAAGCCCTCTCTGTTATAGATACCATTTGTTCTTATGCTTCAATACGA 704
QY 181 ValIleSerAlaIleValThrGlnGlyAsnIlePheAlaThrSerAlaIleArgSerLeuArg 200
| | | | |
Db 705 GTTGTTCGCAAAAACCTCAGGTAATATTTTCCACGTCTGACCTCAGAAAGTCTCCGT 764
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyIleTyrThrIleLeuLeu 220
| | | | |
Db 765 TTCTACAGATCCCTCCGATGTGTCGATGACCGAAGGGAGGACCTTGAATTAATCTG 824
QY 221 GlySerValIleTyrAlaHisSerIleGlnLeuIleThrAlaTyrIleGlyPheLeu 240
| | | | |
Db 825 GGTTCAGTGTATTATGCTCACAGCAGAGAAATTAATCACAGCTGTGTATGATGATTTTGG 884
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluIleAspAlaAsnIleGluPhe 260
| | | | |
Db 885 GTTCTATATTTTGTCTTCTCTGTCTATCTGTGTGAGAAAGATGCAATPAAGAGTTT 944
QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
| | | | |
Db 945 TCTACATATGCAATGCTCTGTGTGTGGGACCAATTACATTGACACATATGGCTATGGA 1004
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QY 281 AsplSerThrProLeuThrTrpLeuGlyArgLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 1005 GACAAACCTCCCTTAACCTTGGCTGGAAAGATGGCTTTCTGACAGCTTTCGACTCTTGGC 1064
QY 301 LLeSerPhePheAlaLeuProAlaGlyLLeuGlySerGlyPheAlaLeuLysValGln 320
DB 1065 ATTTCTTTCTTTGACCTTCCGCGGCACTTCTGGCTCAGGTTTTCATTTAAAGTCAAA 1124
QY 321 GlnGlnHisArgGlnLysHisPheGlnLysArgArgPheProAlaAlaAlaMetLLeGln 340
DB 1125 GAACAAACACCGCCGAAACCTTTGAGAAAGAAAGAACCCAGCTGCACCTCATTCAG 1184
QY 341 CysValTrpArgSerTrpAlaAlaAspGlnLysSerValSerLLeAlaThrTrpLysPro 360
DB 1185 TGAGTTTGGGTAAGTTACGACAGCTGATGAGAAATCTTTCCATTGCACTGGAAACCA 1244
QY 361 HisLeuLysAlaLeuHisPheTrpCysSerProThrAsnGlnLysLeuSerPheLysGlnArg 380
DB 1245 CACTTGAAAGCCTTGCACACCTCGACGCCCTAACCAATGAGAAAGCTTAAGTTTAAAGACCA 1304
QY 381 ValArgMetAlaSerProArgGlyGlnSerLLeLysSerArgGlnAlaSerValGlyAsp 400
DB 1305 GTGGGCACTGGCTAGCCCGACGGGCGCAGAGTATTAAAGCCGACAAAGCTCAGTAGTGAC 1364
QY 401 ArgArgSerProSerThrAspLLeThrAlaGlnGlySerProThrLysValGlnLysSer 420
DB 1365 AGGAGGTCCTCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGGC 1424
QY 421 TrpSerPheAsnAspArgTrpArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
DB 1425 TGGAGCTTCAACGACCCCAACCCGCTTCCGCGCCCTCGCGCCCAAAATTTCTCAGCCA 1484
QY 441 LysProValLLeAspAlaAspThrAlaLeuGlyThrAspAspValTrpAspGlnLysGly 460
DB 1485 AAACCACTGATAGTGTGACACAGCCCTTGCACTGATATGATATGATGAAAGGA 1544
QY 461 CysGlnCysAspValSerValGlnAspLeuThrProProLeuLysThrValLLeArgAla 480
DB 1545 TGCAGGTGATGATGATGATGAGGAAGACTCACCCCACTTAAACTGTCATTCCAGCT 1604
QY 481 LLeArgLLeMetLysPheHisValAlaLysArgLysPheLysGlnThrLeuArgProTyr 500
DB 1605 ATCAGAAATTGAAATTTCACTGTTCGCAAAACGGAAGTTTAAAGGAACATTACCTCCATAT 1664
QY 501 AspValLysAspValLLeGlnGlnLysSerAlaGlyHisLLeAspMetLLeCysArgLLe 520
DB 1665 GATGTAAAGATGTCATTGAACAATATTCGTGGTATCTGACATGATGATGTGAGATAT 1724
QY 521 LysSerLeuGlnThrArgValAspGlnLLeuGlyLysGlnLLeThrSerAspLys 540
DB 1725 AAAAGCTTCAAAACAGCTGTGATCAAAATCTTGGAAAGGCAAAATCAGATCAGATAG 1784
QY 541 LysSerArgGlnLysLLeThrAlaGlnHisGlnThrThrAspAspLeuSerMetLeuGly 560
DB 1785 AAAGAGCGAAGAAATTAACAGCAAAATGAGACCAACAGATCTCAGTATGCTCGGT 1844
QY 561 ArgValValLysValGlnLysGlnValGlnSerLLeGlnSerLysLeuAspCysLeuLeu 580
DB 1845 CGGGTGTCAAGGTGAAAGAAACAGGTACAGTCCATTAATTCAAAGCTGAGCTCTACTA 1904
QY 581 AspLLeTyrGlnGlnValLysValGlnLysSerAlaSerAlaLeuAlaLeuAlaSerPhe 600
DB 1905 GACATCATCAACAGGCTCTTGGAAAGGCTCTGCTCCACCCCTCGCTTGGCTTCAATTC 1964
QY 601 GlnLLeProProPheGlnCysGlnGlnThrSerAspTyrGlnSerProValAspSerLys 620
DB 1965 CAGATCCACCTTTTGAATGTGAACAGACATCTGACATATGAAGCCCTGTGATAGCAAA 2024
QY 621 AsplLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrAsnLLeAla 640
DB 2025 GATCTTTTGGGTTTCCGACAAACAGTGGCTGTATTCAGATCAACATATGCAACATC 2084
QY 641 SerArgGlnLysGlnPheLLeLeuThrProAsnGlnLysPheSerAlaGlnThrPheTyrAla 660

DB 2085 TCGAAGAGGCTGACGTTCAATTGACGCCAAATGAGTTCAGTCCAGACTTTCTACGGG 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProLLeSerGlnSerAspGlySer 680
DB 2145 CTTAGCCCTTAATGTGACAGTCAAGCAACACAGGTGCCAATTAAGTCAAGCGATGCTCA 2204
QY 681 AlaValAlaAlaThrAsnThrLLeAlaAsnGlnLLeAsnThrAlaProLysProAlaAla 700
DB 2205 GCATGGCAGCCCAACACACATTGGCAAAACCAATTAATACGCACTCCAAAGCCAGACGCC 2264
QY 701 ProThrThrLeuGlnLLeProProProLeuProAlaLLeLysHisLeuProArgProGlu 720
DB 2265 CCAACAACCTTACAGATCCCACTCTCTCCGACCATCAAGCATCTGCCCAAGCCAGAA 2324
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerLLeSerAspValThrThrCysLeu 740
DB 2325 ACTCTGACCCCTTAACCTTCAGGCTTACAGAAAGATTTCTGACGCTCACACCTGCTT 2384
QY 741 ValAlaSerLysGlnAsnValGlnValAlaGlnSerAsnLLeThrLysAspArgSerMet 760
DB 2385 GTTGCTCCAGGAAATGTTTCAGTTTGACAGTCAATCTCACAAAGACGCTTCTATG 2444
QY 761 ArgLysSerPheAspMetGlyGlnThrThrLeuLeuSerValCysPrometValProLys 780
DB 2445 AGGAAAGCTTTGACATGGAGAGGAAACCTGTTGTCTGTCTGCTCCATGGTCCGAAG 2504
QY 781 AsplLeuGlyLysSerLeuSerValGlnAsnLLeLysSerThrGlnGlnLysAlaLLe 800
DB 2505 GACTTGGGCAAAATCTTGTCTGTGCAAAACCTGATGAGTGCACCAAGAACTGAATATA 2564
QY 801 GlnLeuSerGlySerGlnSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
DB 2565 CAATCTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2624
QY 821 ArgGlnSerLysLeuPheLLeThrAspGlnGlnValGlyProGlnGlnThrGlnThrAsp 840
DB 2625 AGGGAATCCAAATTTGTTTAACTGATGAAGAGTGGTCCGAAAGACAGAGACAGAC 2684
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGlnAlaAlaPheAlaSerAspSerLeuArg 860
DB 2685 ACTTTTGAATGCGCAGCCAGGAGCTGCGCAGGAAAGCTGCTTGCATCAACATCTTCAAG 2744
QY 861 ThrGlyArgSerArgSerSerGlnSerLLeCysLysAlaGlyGlnSerThrAspAlaLeu 880
DB 2745 ACTGAAAGTCAAGATCATCTCAGACATTTTGAAGCGAGAAAGTCAAGATGCCCTC 2804
QY 881 SerLeuProHisValLysLeuLys 888
DB 2805 AGCTTGCTCATGTCAAACTGAAA 2828

RESULT 5
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kleke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US-10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Alignment Scores:
Pred. No.: 0          Length: 3111
Score: 4547.00       Matches: 888
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%         Indels: 0
DB: 19                  Gaps: 0

US-09-810-796-5 (1-888) x US-10-803-268-3 (1-3111)

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DB      165 ATGAAAGGATGTGGAGTCGGGCGGCGGAGGGTGCTGCTGAACCTCGGACCGCCGAGGGGC 224
QY      21 AaPGlVLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
DB      225 GAGGCGCTGCTACTGCTGGGACCCCGCGGCCACCGCTCGTGCGGCGGCGGCTGCTG 284
QY      41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB      285 AAGGAGAGCGCGCGGCGGCAAGCGGGGCCGCGATGAGCTGCTGGGGAAGCGCTCTCT 344
QY      61 TyrThrSerSerGlnSerGlyArgArgAlaValTyrArgArgValGlnMetTyrLeu 80
DB      345 TACACACAGTACCGACGAGCTGCGCGCCAACTCAATACCGCGGGTGACAACTACCTG 404
QY      81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
DB      405 TACACAGCTGCTGAGAGAGACCCCGCGCTGCGCTTCACTACCAAGCTTTGTTTTCTC 464
QY      101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrIleLeu 120
DB      465 CTGTGCTTGGTGTGCTGATTTTGTTCAGTGTTTTTCACCATCCCTGAGCACAACAAATTG 524
QY      121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB      525 GCGTCAAGTTGCTCTGTGATCTCGAGTTCGTGATGATGTCGCTTTGGTTGAGTTTC 584
QY      141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
DB      585 ATCATTCCGAATCTGGTCTCGGGTCTGCTGTTCGATTAAGAGATGGCAGAGAACTG 644
QY      161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleuIleAlaSerIleAla 180
DB      645 AGGTGTGCTCGAAAGCCCTTGTGTATAGATACCATGTGTTCACTTCCTCAATAGCA 704
QY      181 ValValSerAlaLysThrGlnGlnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB      705 GTTGTTCCTGCAAAAACCTCAGGGTAATATTTTTCACGCTGCACCTGCAAGATCTCCGT 764
QY      201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTyrPheLeuLeu 220
DB      765 TTCCTACACATCTCTCGCATGTGGCCACGAGCAGAGGGAGGACCTTGGAAATTACG 824
QY      221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrIleGlyPheLeu 240
DB      825 GGTTTCAGTGGTTATCTCACAAGCAAGAAATTAATACAGCTTGGTACATAGAGATTTTG 884
QY      241 ValIleuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB      885 GTTCTTAATTTTTCGCTTTCCTGTCTGTCTGTGGGAAAGAGATTAAGATTAAGATTT 944
QY      261 SerThrTyrAlaAspAlaLeuTyrPyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB      945 TCTACATATGCAAGATCTCTCTGTGGGCAACAATTACATTGACAACTATTGGCTATGGA 1004
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QY      281 AspLysThrProLeuThrTyrPheGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB      1005 GACAAAACCTCCCTAACTTGGCTGGAGATTTGCTTCTGCAGGGCTTGCACCTCTTGGC 1064
QY      301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB      1065 ATTCTTCTTTTTCGACTTTCGCGCCGCAATCTTGGCTCAGGTTTGGCATTAAGATACAA 1124
QY      321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB      1125 GACACACACCCCGCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCCAATCTTTCAG 1184
QY      341 CysValIleTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
DB      1185 TGTGTTTGGCTAGTTACGACAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCCA 1244
QY      361 HisLeuLysAlaLeuHisThrCysSerProThrArgGlnLysLeuSerPheLysGluArg 380
DB      1245 CACTTGAAGGCTTTGCACACCTGCAGCCCTACCAATCAGAAAGCTTAAGTTTAAGAGCCA 1304
QY      381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
DB      1305 GTGCCCATGCTAGCCCAAGGGGCCAGAGTATTAAAGCCGACAGCCTCAGTGTGATC 1364
QY      401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
DB      1365 AAGAGGTCCCAAGACCGACATCAAGCCGAGGGCAGTCCACCAAGTCAGAGAGAGC 1424
QY      421 TyrSerPheAsnAspArgThrArgPheArgProSerLeuArgLysLysSerGlnPro 440
DB      1425 TGGAGCTTCAACGACCGAACCCGCTTCGCGCCCTGCGCTCAACAAAGTTCTCAGCCA 1484
QY      441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
DB      1485 AAACAGATGATAGATGCTGACACAGCCCTTGCACTGATGATGATGATGAAAAAGGA 1544
QY      461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
DB      1545 TGCCAGTGTGATGATCAGTGGAGAGACCTCACCCACCACTTAATAAAGCTGATTCGACCT 1604
QY      481 IleArgIleMetLysPheHisValAlaAlaLysArgLysPheLysGluThrLeuArgProTyr 500
DB      1605 ATCAGAAATTATGAATTTTCATGTGCAAAACGAAAGTTTAAGAAACATTACGTCCATAT 1664
QY      501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
DB      1665 GATGAAAAAGATGATGATGAACAAATATCTGCTGCTGATCTCGACATGTTGTGTAATTT 1724
QY      521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
DB      1725 AAAAGCCTTCAAAACAGGTGTGATCAAAATCTTGGAAAAAGGCAAAATCACATCAATAG 1784
QY      541 LysSerArgGluLysIleThrAlaGluHisGlnThrTyrAspAspLeuSerMetLeuGly 560
DB      1785 AAGAGCCGAGGAAATATACAGCAGACATAGACACAGAGCATCTCAGATGTCTCGGT 1844
QY      561 ArgValValLysValGluLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeu 580
DB      1845 CGGGTGTCAAGGTTGAAAAACAGGTACAGTCAATAGATCAAGACTGAGCTGACTTA 1904
QY      581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
DB      1905 GACATCTATCAACAGGTCTTCGAAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATCTT 1964
QY      601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
DB      1965 CAGATCCCACTTTTGAATGTGAACAGACATCTGACATCAAAAGCCCTGTGATGCAAA 2024
QY      621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
DB      2025 GATCTTTGGGTTCCGCACAAAACAGTGGCTTATTCACATCAATCAATGAGCCAAATTC 2084
QY      641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
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Db 2085 TCAGAGAGGCTGCAGTTCATTGACGCCAAATGATGATTCAGTGCAGACTTCTACGCG
QY 661 LeuSerProthmethSerGlnalaThrglnvalProIleSerGlnSerAapGlySer 680
Db 2145 CTTAGCCCTTACTATGACAGCTCAAGCAACAGATGCAATTAAGTCAAAAGCATGGCTCA 2204
QY 681 AlavalalaThraenthrilaleaenGlnIleanthrilaProlyProalaala 700
Db 2205 GCAGTGGCAGCCACCAACACATTGCAACCAATAATACGGCACCCCAAGCCAGCAGCC 2264
QY 701 ProthrThrglnGlnIleProProProleuProalaIlelyshIleuProArpProGlu 720
Db 2265 CCAACAACCTTACAGATCCCACTCCCTCCCAAGCATCAAGCATCGCCAGCCAGAA 2324
QY 721 ThleuHiProbenProalaagIyleuGlnGlnSerIleSerAapValThrThryCyleu 740
Db 2325 ACTCTGACCTTACCTCGAGGCTTACAGAAAGCATTTCTGACGTCACACCTGCTT 2384
QY 741 ValAlaserIysGlnuenaValGlnValAlaGlnSerAenleuthrIysAapArpSerMet 760
Db 2385 GTTGCTCCAGAGAAATGTTCAAGTTGCAAGTCAATCTCAACAGACCTTTCTATG 2444
QY 761 ArgIySerPheAapPheGlyGlyGluThrLeuLeuSerValCysProMetValProlys 780
Db 2445 AGGAAAAGCTTTGACATGGAGAGAAACTGTGTGTCTGTCTGTCCTCCATGTCGCGAAG 2504
QY 781 AapLeuGlyIySerSerLeuSerValGlnAenleuIleArpSerThrgIuGlnAenIle 800
Db 2505 GACTTGGGCAAACTTTGTCTGTGCAAAACCTGATCAGGTCGACGAGGAACGAAATATA 2564
QY 801 GlnLeuSerGlySerGlnSerSerGlySerArpGlySerGlnAapPheThryProlySTP 820
Db 2565 CAACCTTACAGAGAGTGAAGTGAAGTGGCTCCAGAGGACGCAATTTTACCCCAATGG 2624
QY 821 ArgGlnSerIysLeuPheIleThraPheGlnGlnIleValGlyProGlnGlnThraPhe 840
Db 2625 AGGGAATCCAAATGTTTATTAATCTGATGAAGAGTGGGTCCGAGAGACAGAGACAGAC 2684
QY 841 ThrPheAapAlaIalaProGlnProAlaArgGlnAlaIalaPheAaserAapSerleuArg 860
Db 2685 ACTTTTATGATGCCACCGACGCTGCGAGGAAGCTGCTTTCATCAGACTCTCAAGG 2744
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCyleValaagIyGlnSerThraPalaIeu 880
Db 2745 ACTGGAAGCTCAGATCATCTTCAGAGCATTTGTAAGGCAAGAAATGACATGCCCTC 2804
QY 881 SerLeuProhiValIysLeuIys 888
Db 2805 AGCTTGCCTCATGTCAAACTGAA 2828

RESULT 6
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US2002040000A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROUNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNG5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-866-020-1
Alignment Scores:
Pred. No.: 0
Score: 4527.50
Percent Similarity: 99.00%
Best Local Similarity: 98.89%
Query Match: 99.57%
DB: 9
Gaps: 1
US-09-810-796-5 (1-888) x US-09-866-020-1 (1-2694)
QY 1 MetIysAapValGlnSerGlyArgValIleLeuAenSerAlaIalaArgIy 20
Db 1 ATGAAAGATGTGAGTCCGAGCCGAGGACAGGTGCTAACTCGGACCCGACAGGAGC 60
QY 21 AapGlyLeuLeuLeuGlnIleThraAlaIalaThrLeuGlyGlyGlyGlyLeu 40
Db 61 GACGGCTGCTACTGCTGGGCAACCGCGGCACGCTTGTTGTTGGCGGCGGCTG 120
QY 41 ArgGlnSerArgArgIyIysGlnGlnIalaArgMetSerLeuGlnIyIysProleuSer 60
Db 121 AGGGAAGCCGCGGAGAGAGAGGAGGCGGATGAGCTGCTGGGGAAGCCGCTCT 180
QY 61 TyrThrSerSerGlnSerCysArgArgAenValIysTyrArgValGlnAenThryleu 80
Db 181 TACACAGATGACCAAGCTGCGGCGCAACGTCAAGTACCGGCGGAGCAATACCTG 240
QY 81 TyrAenValIleuGlnuArgProArgIyThraIalaPheIleThryAlaPheValPheleu 100
Db 241 TACAACGTGCTGAGAGAGACCCCGGCTGGGCTTCATCAACAGCTTTCGTTTTC 300
QY 101 LeuValPheGlyCyleuIleLeuSerValPheSerThrIleProGlnIleThryIysleu 120
Db 301 CTTGCTTTGCTGCTGATTTTGTCAAGTCTTTCATCATCTCCGAGACACAAATGG 360
QY 121 AlaserSerCyleuLeuIleleuGlnPheValMetIleValValPheGlyLeuGlnIle 140
Db 361 GCTTCAAGTGGCTCTTGAATCTTGAGTTGTAATGATTTGCTTGGTTGGATTC 420
QY 141 IleIleArgIleThraPheArgIyCysCysArgTyrArgIyThraPheGlnIyArgleu 160
Db 421 ATCATTCGAATCTGGATGCTGGGCTTGTGCTGATTAAGAGATGCAAGAAAGACTG 480
QY 161 ArgPheAlaArgIysProPheCysValIleAapThrIleValIleuIleAlaserIleAla 180
Db 481 AGCTTTCGCAAAAGCCCTTCTGTGTATAGATACATTTGTTCTTCAATGCA 540
QY 181 ValIleSerAlaIysThrglnGlnIyAenIlePheAlaThrSerAlaIleuArgSerleuArg 200
Db 541 GTTGTTTCTGCAAAATCAGAGGTAAATTTTGGCAGCTGCACTCAAGATCTCCGT 600
QY 201 PheLeuGlnIleLeuArgMetValArgMetAapArgIyGlyThrThryIysleuLeu 220
Db 601 TTCCTACAGATCTCGCATGAGTGGCATGAGCCGAAGGAGGACACTTGGAAATTAACG 660
QY 221 GlySerValIyThraIleHisSerIysGlnleuIleThraIleThryIleGlyPheleu 240
Db 661 GGTTCAGGTGTTATGCTCACAGCAAGAAATTAACACAGCTTGTATACATAGAAATTTTG 720
QY 241 ValIleuIlePheSerSerPheleuValIyThrLeuValGlnIyAapValAapIyGlnPhe 260
Db 721 GTTCTTATTTTTCCTTTCTTCTTCTGATCTGAGGAAAGAGATCCCAATTAAGATTT 780
QY 261 SerThrTyrAlaAapAlaIleuThryIlePheGlyThrIleThrLeuThrThryIleGly 280
Db 781 TCTACATATGAGAGATCTCTGATGGGCAACATTAATGACAACTATTGGCTATGCA 840
QY 281 AapIyThrProleuThrThryIleGlnIyArgleuLeuSerAlaGlyPheAlaIleuGlnIy 300
Db 841 GACAAAACTCCCTAACTTGGCTGGAAAGATTGCTTTCGACGAGCTTTCACCTCTGGC 900

OY	301	115esrPhepPheAlaleuProAlaGly11leLeuGlySerGlyPheAla1leuLyVaGln	320
Db	901	ATTCCTTCTTGGCACTTCGCGGGCAATCTTGCTCAGGTTTGGCAATTAAAGTACAA	960
OY	321	GlUGlnHISaAGGlnLyGlnHISpHeGluLyVaRgaAGAnProAla1AsnLeu11eGln	340
Db	961	GAACACACCGCCGACAAACCTTTGAGAAAAGAAAGAACCCAGCTGCCACCTCATTAG	1020
OY	341	CysVa11TPaAgSerTYrAla1AaSpGluYsSerVa1Ser11eAla1Th1rTlyPro	360
Db	1021	TGTGTTTGGCGTAAGTTAGCAGCGATAGAAATCTGTTTCCATTGGCAACTGGAAAGCA	1080
OY	361	HisLeuLySA1aLeuHIS1eThCysSerProThr-----	371
Db	1081	CACTTGAAGGCTTCGACACCTCGAGCCCTACCAAGAAAGAAAGGGAAGACATCAAGC	1140
OY	372	AenGlnLyLeuSerPheLySGlnArgVa1ArgMeAla1aSerProArgGlyGlnSer11e	391
Db	1141	AGTCGAAGAGCTAAAGTTTAAAGAGAGAGATGGCCATGGCTAGGCCAGGGGACAGATAT	1200
OY	392	LySserAArgGlnAlaSerVa1GlyAaSpArgAgSerProSerThAaSp1a1eThAlaGlu	411
Db	1201	AAAGGCCAGACGCTTCAGTAGTAGACAGAGATCCCAAGACCCGACATCACAGCCAG	1260
OY	412	GlySerProThrLyVa1GlnYsSer1rPsePheAaAaPaRgThArgPheArgPro	431
Db	1261	GGCAGTCCCAACCAAGCTCAGAAAGAGCTGAGCTTCAACGACCGAACCCGCTTCGGGCC	1320
OY	432	SerLeuAArgLeuLySserSerGlnProLyProVa111eAaP1a1aSpThAla1eGly1	451
Db	1321	TGCGTCCGCTCTCAAAAGTTCTCAGCCAAACCAAGATAGATGCTGACACAGCCCTTGCG	1380
OY	452	ThrAaPaRgVa1TyraSpGluLySGlnCysGlnCysAaRgVa1SerVa1GluAaSpLeuThr	471
Db	1381	ACTGATGATGATATAGTGAAGAAAGAGATGCCAGTGTGATGATATCAGTGGAAGACTCAC	1440
OY	472	ProProLeuLy1eThVa111eArgAla1eArg11eMeLySpPheHISVa1AlaLyArg	491
Db	1441	CCACACCTTAAACGTCATTCGACCTTCAGAAATTAAGAAATTCATGTTGCAAAACGG	1500
OY	492	LySpPheLySGlnThLeuArgProTyraRgVa1LyAaRgVa11eGlnGlnTySerAla	511
Db	1501	AAAGTTTAAGGAAACCTTACGTCACATATATGTAAAGATGTCATTGAACATATTCTGCT	1560
OY	512	GlyHISleuAaPMeLeuCyAaRg11eLySserLeuGlnThArgVa1AaSpGln1leLeu	531
Db	1561	GGTCATCTGGAACATGTTGTGTGAATTAAGACCTTCAAAACAGCTGTGATCAAAATCTT	1620
OY	532	GlyLySGlyGln1eThSerAaSpLySserArgGlyVa11eThAlaGlnHISGlu	551
Db	1621	GGAAAGGGCAATACATCAGATTAAGAAAGGCCGAGAGAAATTAACAGCAACATAG	1680
OY	552	ThrThrAaPaRgLeuSerMeLeuGlyArgVa1LyVa1LyVa1GluYsGlnVa1GlnSer	571
Db	1681	ACCAACAGCGATCTCAGATATGCTCGGTGGGAGGTCAAGTTGAAAAACAGTACAGTCC	1740
OY	572	11eGlnSerLySleuAaSpCyA1eLeuAaSp11eTyrglnGlnVa1LeuArgLySGlySer	591
Db	1741	ATTAAGTCCAAAGCTGGACTGCTTAATTAACATCTATCAACAGGTCCTTCGAAAAGGCTCT	1800
OY	592	AlaSerAla1eAla1aLeuAla1aSerPheGln11eProPheGluCyGlnGln1ThrSer	611
Db	1801	GCCTCAGGCCCTCGCTTGGCTTCATTCCAGATCCCACTTTTGATGTGAACAGACATCT	1860
OY	612	AaPtyrGlnSerProVa1AaSpSerLyAaPLeuSerGlySerAlaGlnAaSerGlyCyS	631
Db	1861	GACTATCAAAAGCCCTGTGATAGCAAAATCTTTCGGGTTCCGCAAAACAGTGGCTGC	1920
OY	632	LeuSerAArgSerThSerAlaAsn11eSerArgGlyLeuGln1nPe11eLeuThProAa	651
Db	1921	TTATTCATCAATCACTAGTGCACAACTTCGAGAGGCCCTCGAGTTCAATCTGACGCCAAT	1980
OY	652	GluPheSerAlaGlnThrPheTyra1aLeuSerProThrMeHISerGlnAlaThrGln	671

Db	1981	GAGTTCAGTCCAGACATCTTCTACGCGCTTAAGCCCTTACTATGCACTCAAGCACAG	2040
Qy	672	ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnTrpIleAlaAsnGlu	691
Db	2041	GTGCCAATTGATCAAAACGATGGCTCAGCAGTGGCAACCCAAACACCATTTGCACAA	2100
Qy	692	IleAsnThrAlaProIleProAlaAlaProThrThreGlnIleLeuProProIlePro	711
Db	2101	ATAAATAGCGACCCCAAGACGACGCCCAACAACCTTAAAGATCCCACTCTCTCCCA	2160
Qy	712	AlaIleIleHisIleuProArgProGluThrLeuHisIleProAsnProAlaGlyLeuGlnGlu	731
Db	2161	GCCATCAAGACATCTGCCCAAGCCAGAAACTCTGACCCCTAAACCTTGACAGCTTACAGAA	2220
Qy	732	SerIleSerAspValIleThrTrpGlyLeuValAlaSerIleGlyLeuAsnValGlnValAlaGln	751
Db	2221	AGCATTTCTGACGTCACACCTGCTGCTTGTGGCTCCAAAGAAAATGTTCAAGTTGCACAG	2280
Qy	752	SerAsnLeuThrIleAspArgSerMetArgIleSerPheAspMetGlyGlyIleThrLeu	771
Db	2281	TCAAAATCTCAACCAAGACCGCTTCTATAGGAAAAGCTTTGACATGGAGAGAAACTCTG	2340
Qy	772	LeuSerValCysProMetValProIleAspLeuGlyIleSerLeuSerValGlnAsnLeu	791
Db	2341	TTGCTCTCTGTCCTCCAGTGGTCCCAAGGACTTGGGCAAACTTTGTTCTGTGCACAAACTG	2400
Qy	792	IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlyIleSerArg	811
Db	2401	ATCAGGTGACCGAGAACTGATATATCAACTTTCAGAGAGTGAAGTCAAGTGGCTCCAGA	2460
Qy	812	GlySerGlnAspPheTrpProIleTrpArgGluSerIleAspPheIleThrAspGluGlu	831
Db	2461	GGCAGCCCAAGATTTTTTACCCCAATGAGGGAATCCAAATGTTTTTAACTGATGAAGAG	2520
Qy	832	ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu	851
Db	2521	GTGGGTCCCAAGACAGACAGACGACACTTTTGATGCCACCGCAGCCTGCCAGGGAA	2580
Qy	852	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys	871
Db	2581	GCTCCTCTTGATCAGACTCTCTAAGCACTGGAAGCTCAAGATCATCTCAGAGCATTTGT	2640
Qy	872	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValIleLeuIys	888
Db	2641	AAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA	2691
RESULT 7			
US-09-810-796-2			
Sequence 2, Application US/09810796			
Patent No. US20020102677A1			
GENERAL INFORMATION:			
APPLICANT: Jeciga, Timothy James			
APPLICANT: ICGen, Inc.			
TITLE OF INVENTION: KCNO5, a NO ₂ US20020102677A1el Potassium Channel			
FILE REFERENCE: 018512-005010US			
CURRENT APPLICATION NUMBER: US/09/810,796			
CURRENT FILING DATE: 2001-10-12			
PRIOR APPLICATION NUMBER: US 60/190,954			
PRIOR FILING DATE: 2000-03-21			
NUMBER OF SEQ ID NOS: 17			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 2			
LENGTH: 2694			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
OTHER INFORMATION: human outwardly-rectifying, voltage-gated			
OTHER INFORMATION: potassium channel KCNO5-1 coding sequence			
NAME/KEY: CDS			
LOCATION: (1)..(2694)			
OTHER INFORMATION: KCNO5-1			
US-09-810-796-2			

Alignment Scores:

Prod. No.:	0	Length:	2694
Score:	4527.50	Matches:	887
Percent Similarity:	99.00%	Conservative:	1
Best Local Similarity:	98.89%	Mismatches:	0
Query Match:	99.57%	Indels:	9
DB:	9	Gaps:	1

US-09-810-796-5 (1-888) x US-09-810-796-2 (1-2694)

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QY 1 MetLysAspValGluSerGlyArgValLeuLeuAnsSerAlaAlaArgGly 20
Db 1 ATGAAGATGTGAGTCGGGCGGGGCGAGGTCGTCTGAATCTCGACGCGCGAGGGC 60

QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 61 GACGGCCTGTACTGCTGGGCAACCGCGCCGCACTGTGTGGCGGGCGGTGGCTTG 120

QY 41 ArgGluSerArgArgGlyLysGlnGlyValArgMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGAGAGCGCGCGGGCAAGCAAGGGGGCCCGAGTGAAGCTCTGGGAAAGCGCTTCT 180

QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCCAGAGCTCGCGCGCAAGTCAAGTACCAGGGGGTGCAGAACTACCTG 240

QY 81 TyrAsnValLeuGlyLysArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACAACTGCTGGAGAACCCCGCGGCTGGGCGTTCATCTACCAACGCTTTCGTTTCTC 300

QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 301 CTGTCTCTTGCTGCTGATTTTGTCACTGTTTCTTCCATCCCTAGACACAAATTTG 360

QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTGGCTCTTGATCTGGAGTTCGTGATGTGTCGTCCTTGGTTTGGAGTTTC 420

QY 141 IleIleArgIleTyrPserAlaGlyCysCysArgArgTyrArgGlyTyrPngInGlyArgLeu 160
Db 421 ATCATTCGAATCTGGTCTCGGGTGTCTGTTCGATAGAGATAGAGATGGCAAGAAAGCTG 480

QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTTGCTGGAAGCCCTTCTGTGTATAGATGCCATGTGTTTATGCTTCAATAGCA 540

QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTTCCTGCAGAAAACCTCAGGGGAAATATTTTGGCCACGTCTGCACACAGATCCGT 600

QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrThrPlyLeuLeu 220
Db 601 TTCTCTCAGATCTCTCGCATGTGCGCATGACCGAAGGGGAGGCACTTGGAATTAATCTG 660

QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaThrPyrIleGlyPheLeu 240
Db 661 GGTTTCAGTGTATATGCTTCACGCAAGAAATTAATCAACACTTGATGATAGAGATTTTG 720

QY 241 ValIleIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTTATTTTTTGCCTTCTTCTGTCTATCTGTGTAAGAAAGTGCATTAAGAGTTT 780

QY 261 SerThrTyrAlaAspAlaLeuTyrPngIleThrIleThrLeuThrThrIleGlyTyrGly 280
Db 781 TCTACATATGCAATGCTCTCTGTGGTGGGCAAAATTAATTAATTAATTAATTAATTAATGA 840

QY 281 AspLysThrProLeuThrTyrPngLysArgLeuLeuSerAlaGlyPheAlaLeuGly 300
Db 841 GACAAAACCTCCCTTAATCTTGGCTGGGAAAGATTTGCTTCTTCTGACGCTTTCAGCTTGGC 900

QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 301 IISerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
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Db 901 ATTCTTTCTTTCACCTTCCTCGCGGCAATTCCTTGAGTTTGCATTAAGATACAA 960
QY 321 GlnGlnHisArgGlnLysHisPheGluLysArgArgAspProAlaAlaLeuLeuIleGln 340
Db 961 GAACAACACCGCGCAGAAACCTTTGAGAAAGAAAGAACCCACACTCCCACTCATTCAG 1020

QY 341 CysValIlePngSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrPngPro 360
Db 1021 TGTGTTGGCGTATGTTACCGACGCTGATGAGAAATCTGTTTCCATTCCATCTGGAAGCCA 1080

QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1081 CACTTGAAGCGCTTGCACACTTCAGCCCTTACCAAGAAAGAACAGGGAGCATCAAGC 1140

QY 372 AsnGlnLysLeuSerPheLysGlyLysArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAGAAAGCTAAAGTTTAAAGAGCGAGTGGCATGGCTTACCCAGGGGCGCAAGATATT 1200

QY 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411
Db 1201 AAGAGCCGACAGACCTCAGTAGTGCACAGAGTCCCCAGACACGACATCACGCCGAG 1260

QY 412 GlySerProThrLysValGlnLysSerTyrPngPheAsnAspArgThrArgPngPro 431
Db 1261 GGCAGTCCCAACCAAGTGCAGAAAGAGCTGAGCTTCAACGACCGAACCCTTCCGGCCC 1320

QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1321 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACGATATGATGCTGACACAGCCCTTGGC 1380

QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1381 ACTGATGATATATATATGATAAAGATGCCAGTGTGATATCACTGGAAGCTCACAC 1440

QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1441 CCACCACTTAAAACTGTCACTTCAGCTATCAGAAATTAATTAATTAATTAATTAATTAAT 1500

QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGlnGlnTyrSerAla 511
Db 1501 AAGTTTAAGAAACGTTACGTTCATATGATGATAAGATGCTATGAAACAATATTTGTCT 1560

QY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1561 GGTCACTGTGACATGTGTGTGATTAATAAGCTTCAAAACAGTGTGATCAATATCTT 1620

QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1621 GGAAAAGGGCAAAATCATCATGATAAGAGCCGAGAAATAAACAACAGAACATGAG 1680

QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1681 ACCACAGACGATCTCGATGCTCGGTGGGTGTCMAAGTTGAAAACAGGTACAGTCC 1740

QY 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1741 ATTAGAGTCCAGAGTGAAGTCTGCTACAGACATCTATCAACAGTCTCTTGCAGAAAGCTCT 1800

QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGlnGlnThrSer 611
Db 1801 GCCTCAGCCCTCGCTTGGCTTCAATCCAGATCCCACTTTGAAAGTGAACAGACATCT 1860

QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1861 GACTATCAAGACCCCTGTGATGACAAAGATCTTTCCGTTCCGCAAAAACAGTGGCTGC 1920

QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1921 TTATCAAGATCAACTAGTCCAAACATCTCGAAGAGCTGCAAGTCAATTGAGGCCAAAT 1980

QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1981 GAGTTCAGTCCAGACTTCTTACGCGCTTACGCCCTTACATGACACAGTCAAGCAACACAG 2040
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QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGln 691
DB 2041 GTGCCAATTAGTCAAAGCCATGGCTCAGCAGTGGAGCCCAACCACTTGGCAACCAA 2100
QY 692 IleAsnThrAlaProIlyProAlaAlaProThrThLeuGlnIleProProProLeuPro 711
DB 2101 ATAAATACGAGCACCCAGCCAGCCAGCCCAACAACTTACAGATCCACCTCTCCCA 2160
QY 712 AlaIleLeuHisIleuProAspArgProGluThrLeuHisIleProAsnProAlaGlyLeuGlnIu 731
DB 2161 GCCATCAACATGTGCCACAGCCAGAAACTCTGCACCTTACCCCTCAGGCTTACAGAA 2220
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLeuGluAsnValGlnValAlaGln 751
DB 2221 AGCATTTCTGACGTCACCACTGCTGCTGTTGCTCCAAAGAAATGTTTCAGGTTGCACAG 2280
QY 752 SerAsnLeuThrIlyAspArgSerMetArgIlySerPheAspMetClyIyIuThrLeu 771
DB 2281 TCMAATCTCACCAAGACCGTTCTATAGAGAAAGCTTTGACATGGAGAGAACTCTG 2340
QY 772 LeuSerValCysProMetValProIlyAspLeuGlyIlySerLeuSerValGlnAsnLeu 791
DB 2341 TTCTCTGTCTGTCCATGTGTCGGAAGACTTGGGAAATCTTTGTCTGTGCAAAACTG 2400
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 811
DB 2401 ATCAGGTCACACGAGAACTGAATATACAACTTTCAGGAGATGACCAAGTGGCTCCAGA 2460
QY 812 GlySerGlyAspPheThrProIlySerTPArgGlySerLeuPheIleThrAspGluGlu 831
DB 2461 GGAGGCCAAGATTTTAACTCCCAATAGAGGAAATCCAAATGTTTAACTGATGAAG 2520
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgIu 851
DB 2521 GTGGGTCCGAGAGACAGACAGACACTTTTGATGCCGACCGACGCTCCAGCGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
DB 2581 GCGGCTTTGCATCAACACTCTCTAAGACTGCGAAGTCAACATCATCAGACATTTGT 2640
QY 872 IlyeAlaGlyGluSerThrAspAlaLeuSerLeuProHisValIlyeLeuIys 888
DB 2641 AAGGCAGAGAAAGTACAGATGCCCTCACCTGCTCATGTCAAACTGAA 2691

RESULT 8
US-10-948-493-1
Sequence 1, Application US/10948493
Publication No. US20050064491A1
GENERAL INFORMATION:
APPLICANT: DWORETZKY, STEVEN I
APPLICANT: RAMANATHAN, CHANDRA S
APPLICANT: TROJANACKI, JOANNE T
APPLICANT: BOISSARD, CHRISTOPHER G
APPLICANT: GRIEKOPF, VALENTIN K
TITLE OF INVENTION: HUMAN KCNJ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
FILE REFERENCE: D0023 DIV
CURRENT APPLICATION NUMBER: US/10/948,493
PRIOR FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: 60/207,389
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2694
TYPE: DNA
ORGANISM: Homo sapiens
US-10-948-493-1

Alignment Scores:
Pred. No.: 0 Length: 2694
Score: 4527.50 Matches: 887

Percent Similarity: 99.00%
Best Local Similarity: 98.89%
Query Match: 99.57%
DB: 21
Gaps: 1
US-09-810-796-5 (1-888) x US-10-948-493-1 (1-2694)
QY 1 MetIlyAspValGluSerGlyArgGlyValIleuAsnSerAlaAlaIlaArgIly 20
DB 1 ATGAAGATGTGAGTCCGAGCGGAGGGGTGCTGAACTCCGACGCCGACAGGGGC 60
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaIleThrLeuGlyIyIyGlyIyGlyLeu 40
DB 61 GACGGCTGCTACTGCTGCGGACCCGCGGCGACAGCTTGGTGGGCGGCGGTGCGCTG 120
QY 41 ArgGlySerArgArgGlyIlyeGlnIyAlaArgMetSerLeuLeuGlyIlyAspProLeuSer 60
DB 121 AGGAGAGCCCGCGGAGACAGGAGGACCCGAGTGAAGCTGTCTGGGAAGCCGCTCTT 180
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValIlyTyrArgArgValGlnAsnThrLeu 80
DB 181 TACACGATGAGCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGCTGACAGAACTACTG 240
QY 81 TyrAsnValIleuGluArgProArgGlyThrAlaPheIleTyrHisAlaPheValPheLeu 100
DB 241 TACACGCTGAGAGAGACCCCGCGCTGGCGTTCATCTACACGCTTTCGTTTCTC 300
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisIleThrIlyLeu 120
DB 301 CTGTGCTTGGTGTGATTTGTGCAGTGTCTTCTACACCTCCGACACACCAAAATTG 360
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValIlyPheGlyLeuGluPhe 140
DB 361 GCCTCAAGTGCCTCTTATCTCGAGTTCGATGATGTGTCGTTGTTGGAGGTTTC 420
QY 141 IleIleArgIleThrSerAlaGlyCysCysCysArgTyrArgGlyTyrGlnIyArgLeu 160
DB 421 ATCATTCGAATCTGTCTGCGGTTGCTGTGTCAATGAGATGAGATGAGCAAGAACTG 480
QY 161 ArgPheAlaArgIlyProPheCysValIleAspThrIleValIleAlaSerIleAla 180
DB 481 AGCTTGTCTCAAAACCTCTCTGTCTTATGATACCACTTGTCTTATGCTTCAATACCA 540
QY 181 ValValSerAlaIlyeThrGlnIyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 541 GTTCTTCTGCAAAACTCAGGCTAATTTTGTCCAGCTGCACACTCAGAACTCCGT 600
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgIyIyThrTrpIlyLeuLeu 220
DB 601 TTCTTACAGATCTCTCGATGCTGCGATGAGCCGAGGAGGAGCACTTGGAAATTACTG 660
QY 221 GlySerValIlyeAlaHisSerIlyGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 661 GGTTCAGTGTATTATGCTACAGACAGAAATTATACAGCTGTTGATAGATTTTGG 720
QY 241 ValLeuIlePheSerSerPheLeuValIlyeLeuValIyIyAspAlaAsnIyGluPhe 260
DB 721 GTTCTTATTTTTCCTCTTCTGCTGTATGTGGGAAAGAGTCAATTAAGAGTTT 780
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 781 TCTACATATGACAGAGCTCTGCGGAGCAATTAATTAATTAATTAATTAATTAATTA 840
QY 281 AspIlyThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 841 GACAAAACCTCCCTTAACTTGGCTGGAGAGATTGCTTTCTGCAGGCTTTCCTTGGC 900
QY 301 IleSerPhePheAlaLeuProAlaGlyIlyeLeuGlySerGlyPheAlaLeuIysValGln 320
DB 901 ATTTCTTTCTTGGCACTTCTGCGGCAATCTTGGCTCAGGTTTGGCTTAAAGTACAA 960
QY 321 GluGlnHisArgGlnIlyHisPheGluIyAspArgAsnProAlaAlaAsnLeuIleGln 340

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Db      961 GAACAAACCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCAACTCATTACG 1020
Qy      341 CysValTTTPArgSerTyrAlaAlaArgGluYsSerValSerTlleAlaThrTTPlyPro 360
Db      1021 TGTGTTGGGCGTGTATACGACGCTGATGAGAAATCTGTTCCATTCCAACTTGAGACCA 1080
Qy      361 HAlaLeuYAlaLeuHAlaThrCysSerProThr----- 371
Db      1081 CACTTGAAGGCTTGGCACACCTGACGCTTACCAAGAAAGAACAGGAGCATCAAC 1140
Qy      372 AengLulYleuSerPheYsguArgValArgMetAlaSerProArgGlyGlnSerTlle 391
Db      1141 AGTCAGAGAGTAAAGTTTAAAGAGCGAGTCCGATGGCTAGCCCAAGGGGCCAGAGATT 1200
Qy      392 YsSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspTlleThrAlaGlu 411
Db      1201 AAGAGCCGACAAAGCCCTCAGAGGTGACAGAGGTCCCAAGCACCAATCAACGCGAG 1260
Qy      412 GlySerProThrLysValGlnYsSerTPSerPheAspAspArgThrArgPheArgPro 431
Db      1261 GGCACTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACGACCAACCGCTTCCGCGCC 1320
Qy      432 SerLeuArgLeuYsSerSerGlnProYsProValTleAspAlaAspThrAlaLeuGly 451
Db      1321 TCGCTCGCCTCAAAAGTTCTCAGCCAAAACAGTGTATGATGCTGACACAGCCCTTGG 1380
Qy      452 ThrAspAspValTyrAspGluYsglyCysGlnCysAspValSerValGluAspLeuThr 471
Db      1381 ACTGAGAGATGATATATATGAAAAAGATGCGAGTGTATCACTGAGAGACCTCCACC 1440
Qy      472 ProProLeuLysThrValTleArgAlaTleArgTleMetLysPheHAlaValAlaYsArg 491
Db      1441 CCACCACTTAAACTGTCACTTCAAGCTATCAAGAAATTTATGAATTTCACTTGGCAAA 1500
Qy      492 YsPheYsGluThrLeuArgProTyrAspValYsAspValTleGluGlnTyrSerAla 511
Db      1501 AAGTTTAAGAAACGTTACGTCATATGATGTAAGAAAGTCTCATTTGAACAAATTTCTG 1560
Qy      512 GlyHAlaLeuAspMetLeuCybaArgTleYsSerLeuGlnThrArgValAspGlnTleu 531
Db      1561 GGTCACTCTGACATGTGTGTGTGATTAATAAAGCCTTCAACAGGTGTGTCAAATTTCT 1620
Qy      532 GlyYsGluGlnTleThrSerAspLysLysSerArgGluYsTleThrAlaGluHAla 551
Db      1621 GGAAGAGGCAATTCATCATCACTAGTAAGAGAGCCGAGAGAAATTAACAGACAACTGAG 1680
Qy      552 ThrThrAspAspLeuSerMetLeuGlyArgValValYsValGluYsGlnValGlnSer 571
Db      1681 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGTACAGTCC 1740
Qy      572 TleGluSerLysLeuAspCysLeuLeuAspTleTyrGlnGlnValLeuArgYsGlySer 591
Db      1741 ATAGAGTCCAAAGCTGACAGCTCCTACTAGCATATCAACAGGTCTCTTGGAAGAGCTCT 1800
Qy      592 AlaSerAlaLeuAlaLeuAlaSerPheGlnTleProProPheGluCysGluGlnThrSer 611
Db      1801 GCTTCAGCCCTCGCTTGGCTTATTCAGATCCCACTTTTGAAGTGAACGACATCT 1860
Qy      612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db      1861 GACTATCAAAAGCCCTGAGTAGCAAAAGATCTTTCGGGTTCGCACAAAAACAGTGCCTGC 1920
Qy      632 LeuSerArgSerThrSerAlaAsnTleSerArgGlyLeuGlnPheTlleLeuThrProAsn 651
Db      1921 TTATTCAGATCAACTAGTGCACACATCTCGAGAGGCTCGAGTTCATTTCAGAGGCAAA 1980
Qy      652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHAlaSerGlnAlaThrGln 671
Db      1981 GAGTTACGTGCCAGACTTTCTACGGCTTAGCCCTACTACTGACAGTCAAGCAACACAG 2040
Qy      672 ValProLysSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrTlleAlaGln 691
Db      2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGAGTGGCGCAACCAACCAATTGCAAAACCA 2100

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Qy      692 TleAsnThrAlaProYsProAlaAlaProThrThrLeuGlnTleProProLeuPro 711
Db      2101 ATAAATATCGGACACCAAGCGACAGCCCAACAACTTATCAATTCACCTCTCTCCA 2160
Qy      712 AlaTleYsHAlaLeuProArgProGluThrLeuHAlaProAspProAlaGlyLeuGlnGlu 731
Db      2161 GCCATCAACATCTGGCCGAGGCGCAAGAACTCTGCACCCCTAACCCCTGACAGCTTACGAA 2220
Qy      732 SerTleSerAspValThrThrCysLeuValAlaSerYsGlnAsnValGlnValAlaGln 751
Db      2221 AGCATTTCTGAGTCAACCACTGCTGCTTGTGCTTCACAAAGAAATGTTACAGTTGCAG 2280
Qy      752 SerAsnLeuThrLysAspArgSerMetArgYsSerPheAspMetGlyGlyGluThrLeu 771
Db      2281 TCAAAATCTCAAGAGACCGTTCTATGAGAAAGCTTTGACATGGAGAGAGAACTCTG 2340
Qy      772 LeuSerValCysProMetValProYsAspLeuGlyYsSerLeuSerValGlnAsnLeu 791
Db      2341 TTGTCTGTCTGTCCATGTGTCGGAAGACCTTGGGCAATCTTGTCTGTGCAAAACCTG 2400
Qy      792 TleArgSerThrGluGluLeuAsnTleGlnLeuSerGlySerGluSerSerGlySerArg 811
Db      2401 ATCAGGTCCAGCGAGAACTGATATACAACTTTCAGGAGTGTGAGTCAAGTGTCTCACA 2460
Qy      812 GlySerGlnAspPheTyrProYsTPArgGlySerTleYsPheTleThrAspGluGlu 831
Db      2461 GGACGCAAGATTTTATCCCAATGAGAGGAATCCAAATTTGTTATTACTGATGAGAG 2520
Qy      832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db      2521 GTGGGTCCGGAAGAGACAGACAGACACTTTGATGCCGACCGGAGCTGCGAGGAA 2580
Qy      852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerTleCys 871
Db      2581 GCTGCTTTCATACAGACTCTTAAGAGACTGGAAGTCAAGATCACTCAGAGCATTTGT 2640
Qy      872 YsAlaGlyGluSerThrAspAlaLeuSerLeuProHAlaValYsLeuYs 888
Db      2641 AAGGCAAGAAAGTACAGATCCCTCAGCTTGCCTCATGTCAAACTGAA 2691

RESULT 9
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Alignment Scores:
Pred. No.: 0 Length: 3137
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 99.57% Indels: 9
DB: 19 Gaps: 1

US-09-810-796-5 (1-888) x US-10-661-629-1 (1-3137)
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Db 1 ATGAAGAGTGGAGTCGGCGCGAGGTCCTGAACTCGGCACCGCCAGGGCG 60
 QY 21 AAGGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
 Db 61 GACGGCTGCTACTGCTGGGGACCCCGGGGCCACCTGGTGCGGGCGGCTGGCTTG 120
 QY 41 ArgGlySerArgArgGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 Db 121 AAGGAAAGCGCGCGGGGCAAGCAGGGGGCGGATGAGCTGGTGGAAGCGCTCTCT 180
 QY 61 TyrThrSerSerGlnSerCysArgArgAlaValLysTyrArgArgAlaGlnMetTyrLeu 80
 Db 181 TACACGAGTAGCCAGAGCTGCCGCGCAACGTCAAGTACCGGGGTGCAAGAACCTTCG 240
 QY 81 TyrAsnValLeuGlyLysArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
 Db 241 TACAACTGCTGGAGAGACCCCGCGCTGGGCTTCATCTACACGCTTCCTGTTTCTTC 300
 QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeu 120
 Db 301 CTGTGCTTGGTGGCTGATTTTGTACGTGTTTCTACATCCCTGAGCAACAATAATG 360
 QY 121 AlaSerSerCysLeuLeuIleLeuGlyLysPheValMetIleValValPheGlyLeuGlyPhe 140
 Db 361 GCCTCAAGTTGCTCTTGATCTCGAGTTCGTGATATGTCGTCTTGGTGGAGTTC 420
 QY 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrProlGlyArgLeu 160
 Db 421 ATCATTCGATCGATCGCTCGGGTTCCTGTTCGATATAGAGAGAGGCAAGGAACACG 480
 QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla 180
 Db 481 AAGTTTGCTCGAAGCCCTTCTGTATATAGATACCATGTTCTTACCTTCAATAGCA 540
 QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
 Db 541 GTTGTTCGCAAAACCTCAGGGTAATATTTTGGCACGCTGCACTCGAAGTCTCCGT 600
 QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
 Db 601 TTCCTACAGATCCTCGCATGCTGGCGCATGAGACCGAAGGGGAGCATTTAGCTG 660
 QY 221 GlySerValValTyrAlaHisSerLysGlyLeuIleThrAlaTyrTyrIleGlyPheLeu 240
 Db 661 GGTTCTAGGTATATCTCACACAGAAATTAATCACAGCTTGATACATAGATTTTGG 720
 QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGlyLysAspAlaAsnLysGlyPhe 260
 Db 721 GTTCTTAATTTTTCGCTCTTCTCTATCTGTGTGAAAGGATGCCAATTAAGAGTTT 780
 QY 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyTyrHisIleThrLeuThrThrIleGlyTyrGly 280
 Db 781 TCTACATATGCAAGATCTCTCTGTGGGGCAACAATTGACATTGACACTATGGCTATGGA 840
 QY 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
 Db 841 GACAAACCTCCCTAATCTGGCTGGGAAAGATGCTTTCGCAAGGCTTTCACCTCCCTGGC 900
 QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
 Db 901 ATTTCTTCTTTCGACTTCTCTGCGGCAATTCCTGAGTTTTCATTTAAAGTACAA 960
 QY 321 GlnGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
 Db 961 GAACACACCGCCAGAAACACTTTGAGAAAGAAAGAACCCAGCTCCCAACCTCATTCAG 1020
 QY 341 CysValTyrArgSerTyrAlaAlaAspGlyLysSerValSerIleAlaHisThrLysPro 360
 Db 1021 TGGTGTGGCGTAGTACGAGCTGATGAGAAATCGTTTCCATTGCAACTGGGAAGCCA 1080
 QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371

Db 1081 CACTTGAAGGCTTGCACACTGCAGCCCTTACCAAGAAACAAAGGGAGCATCAGC 1140
 QY 372 AsnGlnLysLeuSerPheLysGlyLysArgValArgMetAlaSerProArgGlyGlnSerIle 391
 Db 1141 AGTCAGAAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGGCCAGGGGCGCAGATATT 1200
 QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGly 411
 Db 1201 AAGACCCGACAAAGCTTCAGTGTGACAGAGGTCCCAAGCAGCAGCATTCACACCGAG 1260
 QY 412 GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgPro 431
 Db 1261 GGCAGTCCACCAAGCTGACAGAGAGCTGAGCTTCAACGACCAACCCGCTTCGCGCCC 1320
 QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
 Db 1321 TCGTGGCGGCTCAAAAGTTTTCAGCCAAACCAAGTATAGATGCTGACACAGCCCTGGC 1380
 QY 452 ThrAspAspValTyrAspGlyLysGlyCysGlnCysAspValSerValGlyAspLeuThr 471
 Db 1381 ACTGATGATGATATATGATGAAAGAGATGCCAGTGTGATGATTCAGTGGAGACCTCAC 1440
 QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
 Db 1441 CCACCACTTAANAACGTGATTCGACTATCAGAAATTAAGAAATTTTCATGTTCCAAACG 1500
 QY 492 LysPheLysGlyLysThrLeuArgProTyrAspValLysAspValIleGlnGlnTyrSerAla 511
 Db 1501 AAGTTTAAGAAACATTACGTGCATATGATGTAAGATGTCATTTGACCAATATTCGTCT 1560
 QY 512 GlnHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
 Db 1561 GGTCACTCGAGACATGTGTGTGATTAAGCCCTTCAACACGTTGTGATCAAAATTCCTT 1620
 QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGlyLysIleThrAlaGlnHisGly 551
 Db 1621 GGAAGAAAGGCAATATCATCTAGATAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1680
 QY 552 ThrThrAspAspLeuSerMetLeuGlyLysArgValValLysValGlyLysGlnValGlnSer 571
 Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGGGTCAAGAGTTGAAGAACAGGTACAGTTC 1740
 QY 572 IleGlySerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
 Db 1741 ATGAGATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTGGGAAAGCTCT 1800
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlyCysGlyGlnThrSer 611
 Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGCATCT 1860
 QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 1861 GACTATCAAGGCCCTGTGATAGCAAAAGATCTTTCGGGTCCGCAAAACAGTGGCTGC 1920
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLysGlnPheIleLeuThrProAsn 651
 Db 1921 TTATCCAAATCAACTAGTGGCAACATCTCGAAGGCTGCAAGTATATCTTGAGCCAAAT 1980
 QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 1981 GAGTTCAGTGGCCACACCTTTCAGCGCTTAGCCCTACTATGSCAAGTCAAGCAACAGC 2040
 QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
 Db 2041 GTGGCAATTTAGTCAAAAGGATGCTCCACAGTGGCAGGCGCACCAACCATTTCAACCA 2100
 QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
 Db 2101 ATAAATAGGACCCCAAGCGAGAGCCCAACATCTTAACAGATCCACCTCTCTCCCA 2160
 QY 712 AlaIleLysHisLeuProArgProGlyLysHisProAsnProAlaGlyLeuGlnGly 731
 Db 2161 GCCATCAAGCATCTGCCAGGCGCAAGAACTGTGACCCCTAACCTTCGAGGCTTACAGGAA 2220

QY 732 Ser1SerAspValThrThrCysLeuValAlaSerIysGluAsnValGlnValAlaGln 751
DB 2221 AGCATTTCTACGTCACACCTGCTTGTGCTCCAGAGAAATGTTCCAGGTTCACAG 2280
QY 752 SerAsnLeuThrIysAspArgSerMetArgIysSerPheAspMetGlyGlyGluThrLeu 771
DB 2281 TCAAATCTCACCAAGGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAAACTCTG 2340
QY 772 LeuSerValCysProMetValProIleAspLeuGlyIysSerLeuSerValGlnAsnLeu 791
DB 2341 TTGTCTGTCTGCTCCATGTCGCGAAGACTTGGCAATCTTGTCTGTGCAAAACCTG 2400
QY 792 IleArgSerThrGlnGluLeuAsnIleGlnLeuSerGlySerIysSerGlySerArg 811
DB 2401 ATAGAGTCACACGAGACCTGAATATACACTTTCACAGGAGTACATGAGCTCCAGA 2460
QY 812 GlySerGlnAspPheTyrProIysTyrArgGluSerIysLeuPheIleThrAspGluGlu 831
DB 2461 GCGAGCCAGATTTTTACCCCAATGGAGGAATCCAAATTTGTTTAACTGATGAAGAG 2520
QY 832 ValGlyProGlnGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
DB 2521 GTGGGTCGCCAGAGACAGAGACACACTTTGATGTCGCCACCGCAGCTGCCAGGGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
DB 2581 GCTGCTTTGCACTCAGACTCTTCTTAAGGACTGGAAGGTCAGACATCTCCAGACATTTGT 2640
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValIysLeuLys 888
DB 2641 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTCCTCATGTCAAACCTGAAA 2691

RESULT 10
US-09-810-796-1
Sequence 1, Application US/09810796
Patent No. US20020102677A1
GENERAL INFORMATION:
APPLICANT: Jergle, Timothy James
APPLICANT: ICAGEN, Inc.
TITLE OF INVENTION: KCNQ5, a No. US20020102677A1e1 Potassium Channel
FILE REFERENCE: 018512-005010US
CURRENT APPLICATION NUMBER: US/09/810,796
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/190,954
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3071
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
OTHER INFORMATION: potassium channel KCNQ5-1
NAME/KEY: CDS
LOCATION: (10)..(2703)
OTHER INFORMATION: KCNQ5-1
US-09-810-796-1

Alignment Scores:
Pred. No.: 0 Length: 3071
Score: 4523.50 Matches: 886
Percent Similarity: 98.89% Conservative: 1
Best Local Similarity: 98.77% Mismatches: 1
Query Match: 99.48% Indels: 9
DB: 9 Gaps: 1

US-09-810-796-5 (1-888) x US-09-810-796-1 (1-3071)

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QY 21 AspGlyLeuLeuLeuLeuGlnYThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 70 GAGGCTCTTACTGCTGGGACCCGCGGACCCCTTGTGGCGGCGGCTGGCTTG 129
QY 41 ArgGluSerArgArgGlyIysGlnGlyAlaArgMetSerLeuLeuGlyIysProLeuSer 60
DB 130 AGGAGAGCGCGCGGGGCAAGCAGGGGGCCGGATGAGCTGTGGGAAAGCGGCTCTCT 189
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValIysTyrArgArgValGlnAsnTyrLeu 80
DB 190 TACACAGATGAGCAGAGCTCGCGCGCAACGTCAGTACCGCGGGGTGCAGAACTCCCG 249
QY 81 TyrAsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
DB 250 TACAGCTCTGAGAGAGACCCGCGGCTGGGCTTCATCTTACACGCTTTCTTTTCTTC 309
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrIysLeu 120
DB 310 CTGTGCTTTGGTTGCTGATTTTGTCAAGTTTTCATCATCCCTGACACAAATTTG 369
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DB 370 GCTCAAGTTGCTCTTGTGATCCTGAGATTCGATGATGTCGTCCTTGTGTTGAGATTC 429
QY 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrProGlnIysArgLeu 160
DB 430 ATCATTCGATCTGGCTCGGGGTGTCTGTGTCATATAGAGATGGAGAGAACCTG 489
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 490 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATCATTCATTGCTTATGCTTCAATAGCA 549
QY 181 ValValSerAlaIysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 550 GTTGTTCGCAAAACTCAGGGTATATTTTTCACACTGCACTCGAAGTCCCGT 609
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyTyrThrTyrPheLeuLeu 220
DB 610 TTCTTACAGATCTCCGATGGTGGCATGACCGAGGGAGGCACTTGGAAATTAATCTG 669
QY 221 GlySerValValTyrAlaHisSerIysGluLeuIleThrAlaTyrPyrIleGlyPheLeu 240
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DB 730 GTTCTTATTTTTCGCTTCTTCTGTATCTGGTGGAAAGATGCCAATAAGAGTTT 789
QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
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DB 850 GACAAAACTCCCTTAATCTTGGCTGGGAATGCTTTTCGACAGCTTGCATCTCTGGC 909
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QY 321 GlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 970 GAACAACACCGCGCAAAACATTTGAGAAAGAAAGAACCCAGCTGCCAACTCATTTGAG 1029
QY 341 CysValTyrPyrArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTyrPyrPro 360
DB 1030 TGTGTTTGGCGTATGTTAGCAGACTGATGAGAAATCGTTTCATTGCAACCTGGAAGCCA 1089
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
DB 1090 CACTTGAAGGCTTTCACACCTGACAGCTTCAAGAAAGAAACAAGGGAGCATCAACG 1149

QY 372 AenglnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyInserIle 391
Db 1150 AGTCAGAACCTAAGTTTAAAGAGCGAGTCCGATGGTACGCCAGGGGGCCAGGTATT 1209
QY 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411
Db 1210 AAGAGCGGCAAGACCTCAGTGAAGGTGACAGAGGTCCCAAGACCCACATCCAGCGGAG 1269
QY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1270 GGCAGTCCCAACCAATGCGAAGAGCTTGAGCTTCAAGACCGAACCCGCTCCGGCCC 1329
QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaSerThrAlaLeuGly 451
Db 1330 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGTATGATGCTGACACAGCCCTTGCC 1389
QY 452 ThrAspAspValTyrArgGluLysGlyCyArgGlnCyAspValSerValGluLysLeuThr 471
Db 1390 ACTGATGATGTATATATGAAAAAGATGCGACGTGATGTATCACTGGAAGACCTCACC 1449
QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1450 CCACCACTTAAACCTGCTATTCAGAGCTATCAGAAATTATGAAATTTGATGTTGCAAAACGG 1509
QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1510 AAGTTTAAAGAAACCTTACGTCCATGTATGATGTAAAGATGTCTCATTAACAAATTTGCT 1569
QY 512 GlyHisLeuAspMetLeuCyAspArgIleLysSerLeuGlnThrArgAlaAspGlnIleLeu 531
Db 1570 GGTCACTGAGACAGTGTGTGTAATTAAGCCTTCAAAACGTTGTATCAAAATTTCTT 1629
QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGlyLysIleThrAlaGlnHisGlu 551
Db 1630 GGAAGAGGCAATATCATCATCAGTAAAGAGCGGAGGAAAAATACACAGACATGAG 1689
QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1690 ACCACAGACGATCTCAGTATGTCTCGGTCCGGTGTGTCAAGTTGAAAAACAGGTACAGTCC 1749
QY 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1750 ATGAAATCCAGAGTGAAGTGCCTCAGTACATCAATCAACAGGCTCTTGGAAAAAGCTCT 1809
QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCyGluGlnThrSer 611
Db 1810 GCTCAGCCCTGCTTGGCTTATTCAGGTTCCAGCTTTTGAAGTGAACAGATCT 1869
QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1870 GACTATCAAAAGCCCTGTGATGCAAAAGATCTTTCCGGTTCGCGCAAAAACAGTGGCTCC 1929
QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1930 TTATCCAGATCAACTGTGCGCAACATCTGAGAGGCTTGCAAGTTCCTTGAGCCCAAT 1989
QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1990 GAGTTCAAGTCCAGACTTTCTACGCGCTTACGCCCTACATATGACAGTCAAGAAACAG 2049
QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
Db 2050 GTGCCAAATTAATGTCMAAGCATGTGCTGAGAGTGGCCACCAACCACTTGCMAAACCA 2109
QY 692 IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProLeuPro 711
Db 2110 ATAAATACGACCCCAAGCCAGACGCCCAACACTTTACAGATCCCACTCTCTCCCA 2169
QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2170 GCCATCAAGCATGTGCCAGGCGCAAGAACTGTSCACCTAACCTTCAGAGCTTACAGAA 2229
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751

Db 2230 AGCATTTCTGACGTCAACCACTGCTGTGCTCTCAAGAAATGTTCAAGTTGCACAG 2289
QY 752 SerLeuLeuThrLysAspArgSerMetArgLysSerPheAsnMetGlyGlyGlnThrLeu 771
Db 2290 TCAAAATCTCACCAAGACCGTTCATGTAGAGAAACCTTGTGACATGGAGAGAACTCTG 2349
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2350 TTGTCTGTCTGTCCATGATGTGCGAAGACCTTGGCAATCTTTGTCTGTGCAAAACCTG 2409
QY 792 IleArgSerThrGluLysLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
Db 2410 ATCAGGTGACCGAGAACTGATATACACTTTCAGGAGAGTCAAGTGGCTCCAGA 2469
QY 812 GlySerGlnAspPheTyrProLysThrArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2470 GGCAGCCAAAGTTTATTTACCCCAATGAGAGGAGATCAAAATGTTTATATCTGATGAAG 2529
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2530 GTGGTCCCGAAGACAGACAGACACTTTTATGTCGCGACCCGACGCTGCCAGGGA 2589
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2590 GGTGCTTTGATCAGACTCTCTTAAGACTGGAAGTCAACGATCTCATGACAGCATTTGT 2649
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2650 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2700

RESULT 11
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-813-148-1

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: Gaps: 1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyValLeuAsnSerAlaAlaArgGly 20
Db 215 ATGAAGATGTGAGTCCGGCGGAGGGGAGGCTGTAAGTCCGAGCCGCGAGGGGC 274
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40

Db 275 GAGGGCTGCTACTGCTGGGAGACCCGGCCGACGCTTGCTGGCGCGCGGTGGCTG 334
Qy 41 ArgGluSerArgArgGlyLygGlnGlyAlaArgMetSerLeuLeuGlyLyPProLeuSer 60
Db 335 AGGAGAGCGCCGCGGGCAAGAGGGGGCCCGGATGAGCTGCTGGGGAAACCGCTCTCT 394
Qy 61 TyrThrSerSerGlnSerCybArgArgAsnValLysTyrArgArgValGlnaenTyrLeu 80
Db 395 TACACGAGTACGCGAGACTGCGGCGCAAGCTCAAGTACCGGCGAGTGCAGAACTACCTG 454
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheLeuLeuTyrHisAlaPheValPheLeu 100
Db 455 TACACGAGTCTGGAGAGACCCCGGCGCTGGCGGTTCATCAACACGCTTGCTTCTC 514
Qy 101 LeuValPheGlyCybLeuLeuLeuSerValPheSerThrTLeProGlnHisTyrLeu 120
Db 515 CTGTGCTTGGTGGTGGATTTTGTCAGTCTTTTCTACATCCCTGAGCACACAAATTG 574
Qy 121 AlaSerSerCybLeuLeuLeuGluPheValMetLLeValValPheGlyLeuGluPhe 140
Db 575 GCCTCAAGTTGCTTGTGATCTGGAGTGTGATGATGTCGTGCTTGGTTGGAGTTC 634
Qy 141 IleIleArgLLeTrrPseAlaGlyCybCybSerArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 635 ATCATTGCAATCTGCTGCGGGTCTGCTGTTGTCGATATAGAGGATGGCAAGGAAGCTG 694
Qy 161 ArgPheAlaArgLybProPheCybValLLeAspThrLLeValLeuLeuLeuLeuLeu 180
Db 695 AGGTTGCTCGAAAGCCCTCTGTGTATAGATACCATCTTCTTACCTGCTTCAATAGCA 754
Qy 181 ValValSerAlaLysThrGlnGlyAsnLLePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 755 GTTGTCTTCCGAAAACCTCAGGGTAAATTTTGCCAGTCTGCACTCAAGAGTCTCCGT 814
Qy 201 PheLeuGlnLLeLeuArgMetValArgMetAspArgArgGlyGlyThrTrrLybLeuLeu 220
Db 815 TTCTCAGATCCTCCGCGCATGGTGGCGCATGAGCCGAAGGAGGACCTTGGAATTACTG 874
Qy 221 GlySerValValTyrAlaHisSerLybGluLeuLeuLeuThrAlaTrrLyLLeGlyPheLeu 240
Db 875 GGTTGAGTGGTTATGCTCAGCAGCAAGGAATTATCAACACTTGATACATAGGATTTTG 934
Qy 241 ValLeuLLePheSerSerPheLeuValTyrLeuValGluLybAspAlaAsnLybGluPhe 260
Db 935 GTTCTAATTTTTCGTTTCTTCTGATCTGATGAGTGAAGGATGCGCAATGAAGGATTT 994
Qy 261 SerThrTyrAlaAspAlaLeuTrrTrrPGLyThrLLeThrLeuThrThrLLeGlyTrrGly 280
Db 995 TCTACATATGCAATGCTCTCGTGGGGCAACAATTACATTGAACAATTGGCTATGGA 1054
Qy 281 AspLybThrProLeuThrTrrPLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1055 GACAAAACCTCCCTAATTGGCTGGGAGGAAATGCTTCTCAGAGCTTTGCACTCCCTGGC 1114
Qy 301 LLeSerPhePheAlaLeuProAlaGlyLLeLeuGlySerGlyPheAlaLeuLybValGln 320
Db 1115 ATTTCTTCTTTCGACTTCTGCGGCAATCTTGGCTCAGGTTTTCATTTAAAGTACAA 1174
Qy 321 GluGlnHisArgGlnLybHisPheGluLybArgArgAsnProAlaAlaLeuLeuLLeGln 340
Db 1175 GAAACAACCGCCAGAAACACTTTGAGAAAGAAAGAAAGAACCACTGCGCAACCTCATTCG 1234
Qy 341 CybValTrrArgSerTyrAlaAlaAspGluLybSerValSerTrrLeaLLeTrrLybPro 360
Db 1235 TGGTGTGGGTGATGATGCGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1294
Qy 361 HisLeuLybAlaLeuHisThrCybSerProThr----- 371
Db 1295 CACTTGAAGGCTTGGCACCTGCGACCTTACCAAGAAAGAAAGAAAGGAGGAGCATCAAGC 1354
Qy 372 AsnGlnLybLeuSerPheLybGluArgValArgMetAlaSerProArgGlyGlnSerTrr 391
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Db 1355 AGTCAGAGTAAGTTTAAAGAGAGAGTGGCATGGCTAGCCCGAGGGGCGAGATATT 1414
Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspLLeThrAlaGlu 411
Db 1415 AAGAGCGCAACACCTCAGTAGGTGACAGAGGTCCCAAGACCGACATCAACAGCCGAG 1474
Qy 412 GlySerProThrLybValGlnLybSerTrrPsePheAsnAspArgThrArgPheArgPro 431
Db 1475 GGCAGTCCCAACAAATGCGAAGAGCTGAGCTTCAACGACCGAACCCCTCCGGCCC 1534
Qy 432 SerLeuArgLeuLybSerSerGlnProLybProValLLeAspAlaAspThrAlaLeuGly 451
Db 1535 TCGCTCGCCTCAAAAGTTCTCAGCCAAAACGATGATGATGCTGACACAGCCCTTGGC 1594
Qy 452 ThrAspAspValTyrAspGluLybGlyCybGlnCybAspValSerValGluAspLeuThr 471
Db 1595 ACTGATGATGTATATATGATAAAAGATCCCACTGATGATACATGAGAGCCCTCAC 1654
Qy 472 ProProLeuLybThrValLLeArgLLeArgLLeMetLybPheHisValAlaLybArg 491
Db 1655 CCACCACTTAAACTGCTATTGAGCTATCAGAAATTTATGAAATTTATGTTGCAAAACG 1714
Qy 492 LysPheLybGluThrLeuArgProTrrAspValLybAspValLLeGlnGlnTrrSerAla 511
Db 1715 AAGTTTAAAGAAACATTACGTCCATGATGTAAAGATGTCATTGAACAATATCTGCT 1774
Qy 512 GlyHisLeuAspMetLeuCybArgLLeLybSerLeuGlnThrArgValAspGlnLLeu 531
Db 1775 GGTCACTGGACATGTTGTGTGAATTAAGGCTTCAAAACGTTGTATCAAAATCTT 1834
Qy 532 GlyLybGlyGlnLLeThrSerAspLybLybSerArgGluLybLLeThrAlaGlnHisGlu 551
Db 1835 GGAAGAGGCGCAATCACTACATTAAGAAAGCCGAGAAATAACACAGCAACTGAG 1894
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLybValGluLybGlnValGlnSer 571
Db 1895 ACCACAGAGATCTCAGTATGCTCGGTGGGTGTCGCAAGTTGAAGAAACAGGTACAGTCC 1954
Qy 572 LLeGlnSerLybLeuAspCybLeuLeuAspLLeTrrGlnGlnValLeuArgLybGlySer 591
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Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnLLeProProPheGluCybGlnGlnTrrSer 611
Db 2015 GCCTCAGCCCTCGCTTGGCTTCACTTCCAGATCCACCTTTGCAATGTGAACGACATCT 2074
Qy 612 AspTrrGlnSerProValAspSerLybAspLeuSerGlySerAlaGlnAsnSerGlyCyb 631
Db 2075 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTCGGTTCCGCACAAAACAGTGGCTGC 2134
Qy 632 LeuSerArgSerThrSerAlaAsnLLeSerArgGlyLeuGlnPheLLeLeuThrProAsn 651
Db 2135 TTATCCAGATCAACATGTCCAACATCTGAGAGGCTCAGTTCATTCGAGGCGCAAA 2194
Qy 652 GluPheSerAlaGlnThrPheTrrAlaLeuSerProThrMetHisSerGlnAlaTrrGln 671
Db 2195 GAGTTAGTGCACCAAGCTTTCACGCGCTTAGCCCTACATGTCACAGTCAAGGACACAG 2254
Qy 672 ValProLLeSerGlnSerAspGlySerAlaValAlaLLeThrAsnThrLLeAlaGln 691
Db 2255 GTGCCAATTATGTCAAAGCATGGCTCAGCAGTGGCGCACCAACACCACTTGCAACCAA 2314
Qy 692 LLeAsnThrAlaProLybProAlaAlaProThrThrLeuGlnLLeProProProLeuPro 711
Db 2315 ATAAATACGACCAACCAAGCAGAGCCCAACAACATTTACATCCACCTCTCTCCCA 2374
Qy 712 AlaLLeLybHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
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Qy 732 SerLLeSerAspValThrThrCybLeuValAlaSerLybGluAsnValGlnValAlaGln 751
Db 2435 AGCATTTCTGAGGTCAACCACTGCTTGTGGCTCCAAAGAAATGTTTCAGGTTGCACAG 2494

QY 752 SerAsnLeuThrLyAspArgSerMetArgLySerPheAspMetGlyGlyLeuThrLeu 771
DB 2495 TCAAATCTCACCAAGAGCCGTTCTATGAGAAAGCTTTGACATGGAGAGAACTCTG 2554
QY 772 LeuSerValCysPheMetValProLyAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
DB 2555 TTGTCGTCTGTCCTCCATGGCGGAGGAGACTTGGGCAAAATCTTGTCTGTGGCAAACTCTG 2614
QY 792 IleArgSerThrGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
DB 2615 ATCAGGTCGACGAGAACTGATATACAACTTTCAGGAGTGAAGTCAAGTGGCTTCCAA 2674
QY 812 GlySerGlnAspPheTyrProLySTrPAArgLysSerLysLeuPheIleThrAspGluGlu 831
DB 2675 GGCAGCCAGATTTTATACCCCAATGAGGGAATCCAAATTGTTTAACTGTAAGAG 2734
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgLys 851
DB 2735 GTGGGTCGCCGAAAGACAGAGACGACACTTTTGATGCGCACCGAGCTTCCAGGAA 2794
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
DB 2795 GCTGCTTTGTCATCAACTCTCTAAGGACTGGAAGTCAAGTCAATCTCAGAGCAATTGT 2854
QY 872 LysAlaGlyLysSerThrAspAlaLeuSerLeuProIleValLysLeuLys 888
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RESULT 12

US-10-482-834A-55
/ Sequence 55, Application US/10482834A
/ Publication No. US20050074764A1
/ GENERAL INFORMATION:
/ APPLICANT: Mulley, John Charles
/ APPLICANT: Harkin, Louise Anne
/ APPLICANT: Dibbens, Michelle
/ APPLICANT: Wallace, Robyn
/ APPLICANT: Phillips, Hilary Amy
/ APPLICANT: Heron, Sara Elizabeth
/ APPLICANT: Berkovic, Samuel Frank
/ APPLICANT: Scheffer, Ingrid Eileen
/ APPLICANT: Biomedics Limited
/ TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
/ FILE REFERENCE: 1386/17
/ CURRENT APPLICATION NUMBER: US/10/482,834A
/ CURRENT FILING DATE: 2004-01-02
/ NUMBER OF SEQ ID NOS: 173
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 55
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-482-834A-55

Alignment Scores:

Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 21 Gaps: 1

US-09-810-796-5 (1-888) x US-10-482-834A-55 (1-3074)

QY 1 MetLysAspValGlnSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20
DB 215 ATGAAGGATGTGAGTCGGGCGGAGGAGGTCTCTAACTCGGCAACCGCAAGGGGC 274
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 275 GACGGGCTGCTACTGCTGGGCAACCGGCGGCAACGCTTGGTGGCGGCGGTGGCTG 334

QY 41 ArgLysSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 335 AGGAGAGAGCGCGGAGCAAGGAGGAGCGCGAGTGAAGCTCTGAGAAAGCGGCTCTCT 394
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 395 TACAGAGAGTACGACAGGCTGCGGCGCAACGCAAGTACCGGCGGTGCAAGTACCTG 454
QY 81 TyrAsnValLeuGlnLysArgProArgGlyTyrAlaPheIleTyrAsnIleAlaPheValPheLeu 100
DB 455 TACAAAGTCTGAGAGAGACCGCGGCTGGGCTTCACTACCAAGCTTCTGTTTCCCTC 514
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluIleThrLysLeu 120
DB 515 CTGTCTTGGTGGCTTGAATTTTGCAGTGTTTTACCATCTCCGAGACCAAAATTGG 574
QY 121 AlasSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 575 GCTCAAGTGCCTTGAATCTGAGATTCGTAATGATGTGCTTGGTGGAGTTC 634
QY 141 IleIleArgIleTyrPheSerAlaGlyCysCysCysArgTyrArgGlyTyrPglngLysArgLeu 160
DB 635 ATCATTCGAATCTGCTGCGGCTTGTCTGTCTCATATAGAGATGGCAAGAGACTG 694
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 695 AGGTTTGCCTCGAAACCCCTTGTGTATAGTACCATTTGTTATGCTTCAATAGCA 754
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 755 GTTGTTCTGCAAAACTAGGGTAAATTTTGGCAGCTGCACTCGAAGTCTCCCT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
DB 815 TTCCTACAGATCTCGCATGGTGGCGCATGGACCGAAGGGAGGCACTTGAATATTAAG 874
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
DB 875 GGTTACAGTGTATTAAGTCACAGCAAGAAATTAACACAGCTGTGTATACATGATTTTGG 934
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 935 GTTCTTAATTTTTCGTCCTTCTTGTCTATCTGGTGGAAAGATGCCAATTAAGATTT 994
QY 261 SerThrTyrAlaAspAlaLeuTyrPrlGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 995 TCTACATATGAGAGATGCTCGTGGGGGCACAATTAATTGACAACTATGGCATAGGA 1054
QY 281 AspLysThrProLeuThrTyrPleuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 1055 GACAAAACTCCCTTAACTTGGCTGGGAAGATTGCTTTCGACGGCTTGCACCTCTGGC 1114
QY 301 IleSerPhePheAlaLeuProAlaGlyLysLeuGlySerGlyPheAlaLeuLysValGln 320
DB 1115 ATTTCTTTCTTGGACCTTCTGCGGCAATTTCTTGGCTCAGGTTTGCATTAAAGTACA 1174
QY 321 GlnGlnIleAspGlnLysIlePheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1175 GAACAACAACCGCAGAAACACTTTGCAAAAGAAAGAACCCGAGTCCAACTCATTCG 1234
QY 341 CysValTyrPAArgSerTyrAlaAlaAspGlyLysSerValSerIleAlaThrTyrLysPro 360
DB 1235 TGTGTTTGGCGTAAAGTTAGCAGCTGATAGAAATCTGTTCCATTGCAACCTGGAAGCCA 1294
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
DB 1295 CACTTGAAGGCTTTCACACCTGCAAGCTTACCAAGAAAGAACAGGGAAGCATCAAGC 1354
QY 372 AsnGlnLysLeuSerPheLysGlyLysArgValArgMetAlaSerProArgGlyGlnSerIle 391
DB 1355 AGTCAAGAGCTAAAGTTTAAAGAGAGGATGCGCATGCGTACGCCCCAGGGGCAAGATATT 1414
QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411

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Db 1415 AAGAGCCGACCAAGCTCAGTAGGTCAGACAGAGGTCCTCCCAAGCACCAGCATCACAGCCGAG 1474
Qy 412 GlysSerProThryIySvAlGlnlySerTTPSerPheAaAaPArThrAaPheAaPro 431
Db 1475 GGGAGTCCCAACCAAGCAGAAAGAGCTGAGCTTCAACCAAGCCGCTTCCGGCCC 1534
Qy 432 SerLeuAaPheUlySerSergInProLySProValIleAaPAlaAaPThraIaAaGly 451
Db 1535 TCCCTCGGCTCAAAAGTTCTCAGCCAAAACAGTGAATGATCTGACACAGCCCTTGGC 1594
Qy 452 ThrAaPArValIyThrAaPjUlySgIyCySgInCyAaPArValSeryAlaGluAaPLeuThr 471
Db 1595 ACTGATGATGTATATGATGATAAAGATGTCAGTGTGATGTATCATGAGAAAGCTCACCC 1654
Qy 472 ProProLeuUlyThrValIleAaGAlaIleAaGIlEmeUlySphenIySvAlAlaUyAaG 491
Db 1655 CCACCACTTAAACCTGATTCATTCAGAGCTTATCGAAATTAAGAAATTTATGATTTGCAAAACGG 1714
Qy 492 LysPheUlyGluThrLeuAaGProLyAaPArValIyAaPArValIleGluGInTySeraIa 511
Db 1715 AAGTTAAAGAAACATTAACGTCCATATGATGTAAAGATGTCTTGAACAAATTTCTGCT 1774
Qy 512 GlyHleAaAaPMeUleUyCyAaGIlElySeryLeuGInThrAaGValAaPjInIleUy 531
Db 1775 GGTCACTCGACATGTTGTGTAGAAATTAAGCTTCAAAACAGTGTGATCAAAATTTCTT 1834
Qy 532 GlyUyGlyGlnIleThrSeraPlyUySeraGlyUlyAlleThraIaGluHleGlu 551
Db 1835 GGAAGAGGGCAATCACTCATGATTAAGAAAGCCGAGAAATTAACAGAGAACTGAG 1894
Qy 552 ThrThAaPArPLeuSerMeUleUyAaGValIyAaGValIyUySgInValIleUyAaGInSer 571
Db 1895 ACCACAGACGATTCATGATGCTCGGTGGGTGTCAAGTTGAAAAACAGTACAGTCC 1954
Qy 572 IleGlySeryUyAaPcyAaUleUyAaPjIeTyGInGlnIleUyAaGlyUySg 591
Db 1955 ATGAGATCCAGAGCTGAGCTGCTTTCAGACATCTATCAACAGAGTCTTCGGAAGGCTCT 2014
Qy 592 AlaSeraIaAaUaIaAaUaAaSerPheGlnIleProProPheGluCyGluGInThrSer 611
Db 2015 GCTTCAGCCCTCGCTTGGCTTATTCAGATCCACCTTTGAAAGTGAAACGACATCT 2074
Qy 612 AaGlyUyGInSerProValAaPserUyAaPLeuSerSergIleSeraIaGlnAaSerSgIyCyS 631
Db 2075 GACTATCAAAAGCTTGTGATACCAAAAGATCTTCCGGTTCGCCAATAAACAGTGGCTGC 2134
Qy 632 LeuSeraIySerThrSeraIaAaenIleSeraGlyUeUlnPheIleUthrProAa 651
Db 2135 TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTGACAGTTCAATTCGACGCCAAAT 2194
Qy 652 GluPheSeraIaGlnThrPheTyAlaUeUySProThMeChISergInIaIaThrGln 671
Db 2195 GAGTTCAAGTCCAGACTTCTTACGGCTTACGCCCTACTATGACAGTCAAGCAACACAG 2254
Qy 672 ValPProIleSergInSeraPjUySeraIaValAlaIaThraAaThrIleIaAaGln 691
Db 2255 GTGCCAATTATGTCAAAGCGATGCTCAGAGTGGACGCCAACAACCATTCGAAACCAA 2314
Qy 692 IleAaThrAlaAaProLySProAlaAaIaProThrThrLeuGlnIleProProLeuPro 711
Db 2315 ATAAATACGGCAACCAAGCAGACGCCCAACAACTTTACAGATCCACCTCTCCCA 2374
Qy 712 AlaIleUyHleUeUyProAaGProGluThrLeuHleProAaPProAlaGlyUeUlnGlu 731
Db 2375 GCCATACAGATTCGCCAGGCAAGAACTGTACCTCAACCTCAGGCTTAAACGGA 2434
Qy 732 SerIleSeraPValIyThrThrCyUeUyValIaSeryGluAaPValGlnValaIaGln 751
Db 2435 AGCATTTTCACCTCACACCTCTTGTGCTTCCAAAGAAATTTTCAGGTTCACAG 2494
Qy 752 SerAaUeUthrIyAaPArSeraUySeraUySeraPheAaPMeUyGlyGluThrLeu 771
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Db 2495 TCAAATCTCACCAAGGACCGTTCTATGAGAAAAAGCTTTGATGAGGAGAGAACTCTG 2554
Qy 772 LeuSeraValCyAProMeUyValProLyAaPLeuGlyUySeraUySeraValGlnAaUeU 791
Db 2555 TTGTCTGTCTGCCAGTGGTGGCAAGAGACTTGGGAAATCTTTGTCTGTGAAAACTG 2614
Qy 792 IleAaSerThGluGluUeAaenIleGlnLeuSergIySergIySeraGlySeraG 811
Db 2615 ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGAGAGTGAAGTCAAGTGGCTCA 2674
Qy 812 GlySeraGlnAaPheTyProLySProLySeraGlyUySeraUySeraUySeraUy 831
Db 2675 GGCAGCCAAAGATTTTATCCCAATGAGAGGAAATCCAAATTTTATTAATCATGAAGAG 2734
Qy 832 ValGlyProGluGluThrGluThrAaPThrPheAaPAlaIaProGlnProAlaAaGlu 851
Db 2735 GTGGGTCCGAAAGACACAGACAGACACTTTTGAATGCGCAGCCGAGCTCCAGGGAA 2794
Qy 852 AlaIaPheAlaSeraPserUyThrGlyAaGserAaGserSergInSeraIleCyS 871
Db 2795 GCTGCTTTCATCACTCTTAAGAGACTGAAGTCAAGTCAATCATCTCAGAGCATTTGT 2854
Qy 872 LysAlaGlyGluSeraThraPAlaUeUySeraUyProHleValIyUeUyS 888
Db 2855 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2905

RESULT 13
US-10-399-489A-5
; Sequence 5, Application US/10399489A
; Publication No. US20050101004A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: ARGENTIERI, Thomas M.
; TITLE OF INVENTION: METHODS OF SELECTING COMPOUNDS FOR MODULATION OF BLADDER FUNCTION
; FILE REFERENCE: AM100620
; CURRENT FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,078
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/US01/32371
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/281,428
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-489A-5

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 21 Gaps: 1

US-09-810-796-5 (1-888) x US-10-399-489A-5 (1-3074)
Qy 1 MetUyAaPArValGluSeraGlyAaGlyAaGValIleUeUyAaSerAlaIaAaGly 20
Db 215 ATGAAGATGTGAAGTCCGGCCGGGCGAGGGTGTGAACTCGGACGCCCAAGGGGC 274
Qy 21 AaGlyUyLeuUyLeuGlyUyThraGAlaIaThrLeuGlyGlyGlyGlyGlyGly 40
Db 275 GACGGCTGTCTACTCTGTGGGACCCCGCGGCGCAAGCTTGTGTGTGGGGGGGCGGTG 334
Qy 41 ArgGluSeraIyGlyUyGlnGlyAlaIyAaGMeUySeraUyUyAaPLeuSer 60
Db 335 AGGAGAGCCCGCGGGGCGCAAGCAGGGGGCCCGAATGAGCTGTGCTGGAAAGCCGCTCTT 394
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QY 61 TTTThSerSerGlnSerCysArgArGaeValIysTyrArgArgValGlnSerTyrLeu 80
Db 395 TACAGACGTAAGCAGAGCTGCCGCCCAACGTCAAGTACCGGGGGGTGCAGAACTACCTG 454
QY 81 TTTAenValIeuGluArgProArgGlyTTPAlaPheIleTyrHiSaIaPheValI PheLeu 100
Db 455 TACAAAGTCTGAGAGACCCCGCGCTGGCGCTTCATCTACCAACCTTCGTTTTCCCTC 514
QY 101 LeuValPheGlyCysPheIleLeuSerValPheSerThrIleProGlnHisThrIysLeu 120
Db 515 CTGTGCTTTGGTGGTCTTGATTTTGTACAGTCTTTTCTACCATCCCTAGACACACAAATTG 574
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 575 GCCTCAAGTTGCTCTTGATCCTGAGATTGCTGATGATTGCTGTTGGTTGGAGTTC 634
QY 141 IleIleArgIleTTPSerAlaGlyCysCysArgTyrArgGlyTTPGlnGlyArgLeu 160
Db 635 ATCATTCGAATCGTCTGGGGTCTGTCTTCGATATAGAGATGGCAAGGAACTCG 694
QY 161 ArgPheAlaArgIysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 695 AGGTTTGCTCGAAAGCCCTTCGTGTATATAGATACCATTTGTTCTTACGCTTCATAGCA 754
QY 181 ValValSerAlaIysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 755 GTTGTTCGCAAAACTCAGGGTAAATTTTGGCAGCGTCGCACTCAGAAAGTCTCGCT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrTTPylsLeuLeu 220
Db 815 TTCTTACAGATCTCGCATGTGGCCATGGAGCAGAAAGGAGGACCTTGGAATTTACG 874
QY 221 GlySerValValTyrAlaHisSerIysGluLeuIleThrAlaTTPylsIleGlyPheLeu 240
Db 875 GGTTCAGTGGTTATCTCTACAGCAAGAAATTATACAGCTTGATGATAGATTGTTG 934
QY 241 ValIleuIlePheSerSerPheLeuValTyrLeuValGluIysAspAlaAsnIysGluPhe 260
Db 935 GTTCTTAATTTTTTCGCTTTCTCTGTCATCTGTGGAAAGATGCCAATTAAGAGTTT 994
QY 261 SerThrTyrAlaAspAlaLeuTTPylsTTPylsIleThrLeuThrThrIleGlyTyrGly 280
Db 995 TCTACATTAATGCAAGATCTCTGTGGTGGGACAAATTATGCAACTATTTGGCTATGGA 1054
QY 281 AspIysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1055 GACAAAACTCCCTTAACCTTGCGTGGGAAGATTCTTCTGCAAGCTTTCACCTCTGGC 1114
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuIysValGln 320
Db 1115 ATTTCTTTCTTGGCACTTCTCGCGCATTTCTTGCGTCAAGTTTTCATTTAAAGTACAA 1174
QY 321 GlnGlnHisArgGlnIysHisPheGlnIysArgArgAsnProAlaIleAsnIleGln 340
Db 1175 GAACAAACACCGCGGAAACCTTTGAGAAAGAGAAAGAACCCAGCTGCAACCTCATTCAG 1234
QY 341 CysValTTPArgSerTyrAlaIleAspGluIysSerValSerIleAlaThrTTPylsPro 360
Db 1235 TGTGTTTGGCGTATGTAACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAAGCA 1294
QY 361 HisLeuValAlaLeuHisThrCysSerProThr----- 371
Db 1295 CACTTGAAAGCCTTGACACCTGCAACCTTACCAAGAAAGAAACAAAGGGAGACATCAAGC 1354
QY 372 AasnGlnIysLeuSerPheIysGluArgValArgMetAlaSerProArgIlyGlnSerIle 391
Db 1355 AGTCAAAGCTAAAGTTTAAAGAGCGAGTGGCATGGTCAAGCCCGAGGCGCAAGATATT 1414
QY 392 IysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGln 411
Db 1415 AAGAGCCGACAAAGCCTCAGTAAAGTGAAGAAGGTCCCAAGACCGACATTCACAGCCGAG 1474

QY 412 GlySerProThrIysValGlnIysSerTTPSerPheAsnAspArgThrArgPheArgPro 431
Db 1475 GGCACTCCCAACCAAGGTGCAGAAAGCTGAGCTTCACAGACGAAACCGCTTCCGGCCC 1534
QY 432 SerLeuAlaGluLeuIysSerSerGlnProIysProValIleAspAlaAspThrAlaLeuGly 451
Db 1535 TCGTCGCGCTTCAAAAGTTCTCAGCCAAACCAAGATAGATGCTGACACACGCTTGGCC 1594
QY 452 ThrAspAspValTyrAspGluIysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1595 ACTGATGATGATATAGTAAAGAAAGATGCCAGTGTGATGATCTAGTGGAGACCTCAC 1654
QY 472 ProProLeuIysThrValIleArgAlaIleArgIleMetIysPheHisValAlaIysArg 491
Db 1655 CCACCACTTTAAACGTGATTCGAGCTATCAGAAATTATGAATTTTCATGTTCAAAACCG 1714
QY 492 IysPheIysGluThrLeuArgProTyrAspValIysAspValIleGlnGlnTyrSerAla 511
Db 1715 AAGTTTAAAGAAACATTACGTCAATATGATGTAAAGATGTCATTGAAACAATATTCGCT 1774
QY 512 GlyHisLeuAspMetLeuCysArgIleIysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1775 GGTCACTCGACATGTTGTGTAGATTTAAACCTTCAAACACGCTTGATCAAAATTCTT 1834
QY 532 GlyIysGlyGlnIleThrSerAspIysIysSerArgGluIysIleThrAlaGluHisGlu 551
Db 1835 GGAAGAAAGGCAAAATCATCATGATTAAGAAAGCCAGAGAAATTAACAGCAGAAACATGAG 1894
QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValIysIysValGluIysGlnIleGlnSer 571
Db 1895 ACCACAGACGATCTAGTATGCTGGTGGGGTGCAGAGTTGAAACAGGTTACAGTCC 1954
QY 572 IleGlnSerIysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgIysGlySer 591
Db 1955 ATGAAATCCAAAGCTGAGCTGGCTTATAGACATCTATCAACAGGCTCTCGAGAAAGCTCT 2014
QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGluGlnThrSer 611
Db 2015 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 2074
QY 612 AspTyrGlnSerProValAspSerIysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 2075 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCCGCACAAACAGTGCGTC 2134
QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgIysLeuGlnPheIleLeuThrProAsn 651
Db 2135 TTATCAATCAATCAATGAGCCAAATCTCGAGAGGCTCGAGTTCAATCTGACGCCAAT 2194
QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 2195 GAGTTCAGTGCCCAACTTCTTACCGCGCTTAGCCCTTACTATGCAACAGTCMAAGCAACAG 2254
QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
Db 2255 GTGCCAATTAGTCAAAGGATGGCTCAGACAGTGGAGGCCACCAACCATTTGCCAAACCA 2314
QY 692 IleAsnThrAlaProIysProAlaIleProThrThrIleuGlnIleProProLeuPro 711
Db 2315 ATAAATTAAGGACCCCAAGCCAGAGCCCAACCAACTTACAGATCCACCTCTCCCA 2374
QY 712 AlaIleIysHisLeuProArgProGluThrIleHisProAsnProAlaGlyLeuGlnGlu 731
Db 2375 GCCATCAAGCATCTGCCCAGGCGCAAACTCTGACCCCTTAACCTGCAAGGCTTACAGGA 2434
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerIysGluAsnValGlnValAlaGln 751
Db 2435 AGCATTTCTGACGTACACACCTGCTTGTGCTTCCAAAGAAATGTTCAAGTTGACAG 2494
QY 752 SerAsnLeuThrIysAspArgSerMetArgIysSerPheAspMetGlyGlyIleThrIleu 771
Db 2495 TCAATATCTCAACCAAGAGACGTTCTATGAGAAAGCTTTGACATGGAGAGAAACTCTG 2554
QY 772 LeuSerValCysProMetValProIysAspLeuGlyIysSerLeuSerValGlnAsnLeu 791

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Db 2555 TTGTCGTGTGTCCACGATGTCGGAAGGACTTGGGCAAACTTGTCTGTGCAAAACCTG 2614
Qy 792 11eArSerThrGluGluLeuAen11eGlnLeuSerGlySerGluSerSerGlySerArg 811
Db 2615 ATAGGTCGACCGACGAACTGAATATACACTTCAGGGAGTACGACAACTGCTCCAG 2674
Qy 812 G1ySerGlnApePheTyPProLySTPArgGluSerLySerLysPheHeiLeuApeGluGlu 831
Db 2675 GCGAGCCAAATTTTATCCCAATGAGGAAATCCAAATTTGTTATTAAGTATGAGAG 2734
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAla1a1aProGlnProAlaArgGlu 851
Db 2735 GTGGGTCGCCAAGACAGACAGACACTTTGATCCGACCGAGCTCCGACGGAA 2794
Qy 852 AlaAlaPheAlaSerApeSerLeuArgThyGlyArgSerArgSerGlnSerIleCys 871
Db 2795 GCTGCTTGGCACTCACTCTTAAGACCTGAAAGTCAGACATCACTCAGAGCATTTGT 2854
Qy 872 LysAlaGlyGluSerThrApeAlaLeuSerLeuProHisValLysLeuLys 888
Db 2855 AAGCGAGAAAGTACAGATGCCCTCAGCTTGCATGTCAAACTGAAA 2905

RESULT 14
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Scagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14195,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 11720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 34624, 64624, 84237, 8912, 2866,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MP102-018P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
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; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55
Alignment Scores:
Pred. No.: 9,84e-198 Length: 2335
Score: 2007.50 Matches: 434
Percent Similarity: 65.32% Conservative: 82
Best Local Similarity: 54.94% Mismatches: 133
Query Match: 44.15% Indels: 141
DB: 17 Gaps: 16

US-09-810-796-5 (1-888) x US-10-353-690-55 (1-2335)
Qy 8 ArgGlyArgValLeuLeuAenSerAla1a1aArgGlyAspGlyLeuLeuLeuLeuGly 27
Db 127 CCGGGACGCCCGCCCGGACGACTAGTGGCGCTCACCGC----- 165
Qy 28 ThrArgAla1a1aThrLeuGlyGlyGlyGlyLeuArgGluSerArgArgLys 47
Db 166 ---CGTGCAGACGAAACAGGCGAGCGGG-----CGGGGCGG 201
Qy 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
Db 202 CTCGCCCGCGCGCTCGCTCGCTCGCTCGCGAGCCCGCGCGCGCGCGCGCGCTCCG 261
Qy 60 -----SerTyThrSerSerGlnSerCysArgArgAsnValLysTy 73
Db 262 GCCGGGCTCGCGCTCGCGCTCGCGCTCGCGCGCGCGCTCGCGCGCGCGCGCGCTA 321
Qy 73 rArgArgValGlnAenTyLeuTyArgAsnValLeuGluArgProArgGlyTyrAlaPhe11 93
Db 322 CCGCGCGCTCGCGAACTGGGTCTTACAGCTGCTGAGCGCGCGCGCGCGCTGGGCTTGT 381
Qy 93 eTyHisAlaPheValPheLeuLeuValPheGlyCysLeu11eLeuSerValPheSerTh 113
Db 382 CACACACGCTTCATATTTTCTGCTGCTTACGCTGCGCTGCGCTGCTGCTGCTGCTG 441
Qy 113 r11eProGluHisThrLysLeuAlaSerSerCysLeuLeu11eLeuGluPheValMet11 133
Db 442 TATCCAGGACGACCGAGCACTTGCACAAAGGTCTCCCTCATCTTGAATTCGTATGAT 501
Qy 133 eValValPheGlyLeuGluPhe11e1eArg11eTyrPheSer1a1aGlyCysCysArgTy 153
Db 502 CGGCTTTCGCGCTGAGTACATCGCGGCTGCTGCTGCGCGAGTGTGCTGCGCGTCA 561
Qy 153 rArgGlyTyrGlnGlyArgLeuArgPheAlaArgLysPropheCysVal11eAspThr11 173
Db 562 CCGAGGATGCGAGGATCGCTTCCGCTTCCAGAAAGCCCTTCTGTGTCATGACATTAT 621
Qy 173 eValLeu11eAlaSer11eAlaValSer1a1aLysThyGlnGlyAen11ePheAlaTh 193
Db 622 CGTGTTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 681
Qy 193 rSerAlaLeuArgSerLeuArgPheLeuGln11eLeuArgMetValArgMetAspArgAr 213
Db 682 GTCCGCGCTGCGAGATGCGCTTCTCGAGATCTTCCGCAAGTGTGCGCATGACCGCG 741
Qy 213 gGlyGlyThrTyrLysLeuLeuGlySerValTyAlaHisSerLysGluLeu11eTh 233
Db 742 CCGCGGCGACCTGGAAGCTGCTGGCTCAAGTGTCTACCGGCAACGAGACTGATCAC 801
Qy 233 rAlaTyrTy11eGlyPheLeuValLeu11ePheSerSerPheLeuValTyTyLeuValG1 253
Db 802 CCGCTGTGACATCGGGTCTCTGTGCTCATCTTCCCTTCCGTGCTTACCTGCGCCA 861
Qy 253 uLysAspAlaAenLysGluPheSerThrTyArgAlaAspAlaLeuTyrTPArgLysTh11eTh 273
Db 862 GAAAGAGCCCACTCGACTTCTCTCTCAACCGACATCGCTCTGTGGGAGCAATTHC 921
Qy 273 rLeuThrThr11eGlyTyArgLysPheLysThrProLeuThrTyrLeuGlyArgLeuLeu 293
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Db	922	ATTGACAAACATCGGCTATTGGGACAAACACCCGACACATGTCGGCGGACAGTCTCGC	981
Oy	293	ralaglyPhealaleuleuGlyIleSerPhePhealaleuProalagIyIleleuGlyse	313
Db	982	TGCTGGCTTGGCTTACCTAGGGCATCTCTTTCTTTGCTCGCTGGCATCTTAGGCTC	1041
Oy	313	rgIyPhealaleuleuValGInGlnGlnHIsArgIlnlyshIshPheGlnulysArgArgAs	333
Db	1042	CGGCTTTGCCCTTGAAGTCTCCAGACACACCCGCAAGAACCTTCGAGAAACGGAGAT	1101
Oy	333	nProAlaAlaamleuIleGInCysValTTPArgSerTyralaalaApe---GluIysse	352
Db	1102	GCCGGACACCAACCTCATCCAGGCGCTCGGGCGCTGTACTCCACCGATATGAGCGGAGC	1161
Oy	352	rValserIlelaThrTP-----	358
Db	1162	CTACCTGACAGCCACTGTGTACTACTATGACAGTATCTCTCCATCTTCAAGAGACTGGC	1221
Oy	358	-----	358
Db	1222	CCTCTTTGTAGACGTGCAACGGGCGCCGCAATGGGGGCGTACGGGCCCTTGAGAGTGG	1281
Oy	359	-----LysProHIsleuIlysalaleuHIsTh	367
Db	1282	GCGGCGCCGGTACCCGACGAGACACCTCCCGTTACCCGCGCGCTTGCACTCGCACCG	1341
Oy	367	r-----CysSerProThrAsnGlnIlyIleuSerPheIysGlnArgVa	381
Db	1342	GCCGGGACGACACTCTCTTGTGCTCCCTGGGGAAAGACGCCGATGGGACATCAAGACCGAT	1401
Oy	381	lArgMetAlaSerProArgIlyGlnSerIleIysSerArgIn---AlaSerValG	399
Db	1402	CCGCTATGGGACCTCCACGCGGACGCGGCTCTTCCACAGACGACGCTGCACTCCAAC	1461
Oy	399	yAspArgArgSerProSerThrAspIleThraIagIuIy---SerProThrIysValG	418
Db	1462	AATGCCCACTCCCAAGACGACGACAGTGGGTAGGACCAACCCCCACCAAGATGCA	1521
Oy	418	nIlySerTrpSerPheAsnAspArgThrArgPheArgProSerIleuArgIleuIysSerSe	438
Db	1522	AAAGAGCTGAGCTTCATGACCCGACCCGCTTCGGGCACTCTGAGACTC-----	1573
Oy	438	rgInProIyProValIleAspAlaAspThrAlaIleuGlnThraAspAspValTyraAspG	458
Db	1574	-----AAACCCCGCACCTCTGCTGAGAGATGC--CCCTCAGAGAAATGACAGAGA	1623
Oy	458	uIlysgIyCysGInCysAspAspAlaSerValGlnAspIleuThrProProIeulysThValI	478
Db	1624	GAAAGAGTACACAGTGTGAGCTCAAGGTGAGACATCATGTGCTGTGAAAGACGTAT	1683
Oy	478	eArgAlaIleArgIleMetIlyPheHIsValAlaIlyArgIlyPheIlysgIuThrIleuAr	498
Db	1684	CCGCTCCATCAGGATTCCTCAAGATTCCTGTGGCCAAAGAAATTCAGAGAGACATCGCG	1743
Oy	498	gProIyTrAspValIlyAspAspValIleGlnGlnIlyTyrSerAlaGlnHIsIleuAspMetLeuCy	518
Db	1744	ACCGTACACACTGAAAGACGTCATTGACAGTACTCAGACAGGCCACTCGACATGCTGGG	1803
Oy	518	sArgIleIysSerIeugInThrArgValAspGlnIleleuGlnIlysgIyGlnIleThrSe	538
Db	1804	CCGATCAACAGGCTCGCAAACTCGGGTGAGCAAAATTTGGTGGCGGG-----CCCGG	1857
Oy	538	rAspIlyIysSerArgInIy-----LysIleThraIagIuHIsGlnuThrThrAspAs	555
Db	1858	GGAACGAGAGGCGCCGGAGAAAGGCGACAAAGGGCCCTCCACCGCGGAGGTGGATGA	1917
Oy	555	pIeuserMetLeuArgValIlyValIlyValGlnIlysgIlnValGInserIleGInserIy	575
Db	1918	AATCAGCATGATGGGACGCTGTGTCATAGCTGAGAAACAGAGGTGACGTCACTGAGACAA	1977
Oy	575	gIeuaAspCyIleuIeuaAspIleTyrgInGlnIValIeuaArgIlysgIysAlaSerAlaIe	595
Db	1978	GCTGGACCTGTGTGGCTTCTATCCGCTGTGCTGGCTGTGACACTTGAGC-----	2032

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QY      595 uAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAerTYrgInSe 613
      :::::
Db      2033 -ACCTGGGCGCGCGTGAAGATGTCCTCTGTGACCCCGACATCACTCCGACTACACAG 2090
QY      615 rProValaSerLeuAerPLeuSerGlySerAlaGlnaSerSerGlyCysLeuSerArgSe 633
      :::::
Db      2092 CCCTGTGGACACAGAGAGATATCTCCGTCTCCGACAGACGCTACG---ATCTCCGCTC 2144
QY      635 rThrSerAlaAenIleSerArgGlyLeuGlnPheIleuThrProaGlnPheSerAl 655
      :::::
Db      2149 GGTCAACACACCAACATGACTGAGCGG----- 2177
QY      655 aGlnThrPheTYrAlaLeuSerProThrMechIsSerGlnAlaThrGlnValProIleSe 675
      :::::
Db      2174 -----ACTTC 2177
QY      675 rGlnSerAerGlySerAlaValAlaAlaThrAerThrIleAlaAenGlnIleAenThrAl 695
      :::::
Db      2179 TCAGAGAGCAGGGGAGCACA-----CGGCGACG 220
QY      695 aProLYsProAlaAlaAlaProThrThLeu-GlnIleProProProProAlaIleLYsH 715
      :::::
Db      2206 CCGCGCGAGCTGGGCGCTCCGACCTGCGCCCTGAGAGGCTCCGACATCTCTCGATTGAAC 226
QY      715 iLeuProArProGlnThrLeuHis 723
      :::::
Db      2266 CACTCCCTCACGGGAGAGACACGAC 2291

RESULT 15
US-10-850-928-1
: Sequence 1, Application US/10850928
: Publication No. US20050037460A1
: GENERAL INFORMATION:
: APPLICANT: JENTSCH, Thomas J.
: TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
: FILE REFERENCE: 2815-127PUS2
: CURRENT APPLICATION NUMBER: US/10/850,928
: CURRENT FILING DATE: 2004-05-20
: PRIOR APPLICATION NUMBER: 09/492,361
: PRIOR FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 41
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 2335
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: gene
: LOCATION: (1)..(2335)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (83)..(2170)
US-10-850-928-1

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Score:             2007.50             Matches:      434
Percent Similarity: 65.32%             Conservative:    82
Best Local Similarity: 54.94%             Mismatches:     133
Query Match:       44.15%             Indels:         141
DB:                21                  Gaps:          16

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 08:19:35 : Search time 337.985 Seconds
(without alignments)
14867.549 Million cell updates/sec

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Perfect score: 3071

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Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2890.8	94.1	3111	4	US-09-825-147-3	Sequence 3, Appl1
3	2857.4	93.0	3074	4	US-09-813-148-1	Sequence 1, Appl1
4	2635.4	85.8	2772	4	US-09-825-147-1	Sequence 1, Appl1
5	518	16.9	2196	4	US-09-949-016-1823	Sequence 1823, Ap
6	518	16.9	2335	4	US-09-492-361-1	Sequence 1, Appl1
7	517.6	16.9	2273	3	US-09-177-650-88	Sequence 88, Appl
8	511.6	16.7	2169	3	US-09-105-058C-22	Sequence 22, Appl
9	509.8	16.6	582	4	US-09-495-050A-303	Sequence 303, App
10	465.4	15.2	896	3	US-09-105-058C-1	Sequence 1, Appl1
11	463.6	15.1	2814	3	US-09-177-650-90	Sequence 90, Appl
12	460.8	15.0	2565	3	US-09-105-058C-26	Sequence 26, Appl
13	460.8	15.0	2914	3	US-09-177-650-6	Sequence 6, Appl1
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41	134.6	4.4	251	4	US-09-495-050A-296	Sequence 296, App
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45	84.8	2.8	649	3	US-09-177-650-118	Sequence 118, App

ALIGNMENTS

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; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
; FILE REFERENCE: 2815-0136P
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1

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Db 2641 AAGGACGAGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAACTGAATTAATTTCTT 2700
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|
QY 2710 CATTTTCTTTCAGGAGTACAGATTTCTTTAGCCATACATCATTTGATGAACTATTTTCG 2769
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Db 2701 CATTTTCTTTCAGGAGTACAGATTTCTTTAGCCATACATCATTTGATGAACTATTTTCG 2760
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|
QY 2770 AAGCCCTTTAAAGTTGAAATTTGCAAGATGCGGAGAACTGAAGGACGTTTATA 2829
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|
Db 2761 AAGCCCTTTAAAGTTGAAATTTGCAAGATGCGGAGAACTGAAGGACGTTTATA 2820
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QY 2830 AGCCCGTTTACCTTTTAATTCATGAAATGCAATGTTTGGATGCTTAAATTCAGAGT 2889
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Db 2821 AGCCCGTTTACCTTTTAATTCATGAAATGCAATGTTTGGATGCTTAAATTCAGAGT 2880
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|
QY 2890 GCATCGACATTAACCCCTCATTTAGTAATGTATCTTGAATTTAAAGCTTGAGAAACCA 2949
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|
Db 2881 GCATCGACATTAACCCCTCATTTAGTAATGTATCTTGAATTTAAAGCTTGAGAAACCA 2940
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|
QY 2950 AACACAGTATGCTATGCGGAGTATGATATGTCAGATTTAGGTCATTTAGAGATTTTG 3009
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Db 2941 AACACAGTATGCTATGCGGAGTATGATATGTCAGATTTAGGTCATTTAGAGATTTTG 3000
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|
QY 3010 ACACTGATTTTGAATTTATGGAAGTAACACCTTCAAAATTTCA 3053
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|
Db 3001 ACACTGATTTTGAATTTATGGAAGTAACACCTTCAAAATTTCA 3044
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RESULT 2
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiehe, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sanders, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: Lex-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Query Match 94.1%; Score 2890.8; DB 4; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

QY 1 GGCAGCGGATGAAGATGTGAGTCCGGCCGGGAGAGGATGCTGTAAGCTCGGACGCC 60
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Db 156 GGCAGCGGATGAAGATGTGAGTCCGGCCGGGAGAGGATGCTGTAAGCTCGGACGCC 215
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QY 61 GCCAGGGGCGACGGCTCTACTGCTGGGACCCCGCGGCGACGCTTGGTGGCGGCGC 120
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Db 216 GCCAGGGGCGACGGCTCTACTGCTGGGACCCCGCGGCGACGCTTGGTGGCGGCGC 275
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QY 121 GGTGCTTGAAGAGAGCCGCCGGGGCAAGCAGAGGGGCCCGGATGAGCTGCTGGGAGG 180
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Db 276 GGTGCTTGAAGAGAGCCGCCGGGGCAAGCAGAGGGGCCCGGATGAGCTGCTGGGAGG 335
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QY 181 CGGCTCTTTTAAACGAGTATGAGCCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGTCAG 240
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Db 336 CGGCTCTTTTAAACGAGTATGAGCCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGTCAG 395
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QY 241 AACTACTGTAACACGTGCTGAGAGAACCCCGGGCTGGGCGTTTCAATCAACACGCTTTC 300
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Db 396 AACTACTGTAACACGTGCTGAGAGAACCCCGGGCTGGGCGTTTCAATCAACACGCTTTC 455
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QY 301 GTTTTCTCCCTTGTGGTTGCTTGAATTTTGTCAAGTATTTTCTCAATCCCTGAGCAC 360
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Db 456 GTTTTCTCCCTTGTGGTTGCTTGAATTTTGTCAAGTATTTTCTCAATCCCTGAGCAC 515
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QY 361 ACAAAATGGCCCTCAAGTTGCTCTTGAATCTGAGATTCGTATGATGATGATGATGATGAT 420
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Db 516 ACAAAATGGCCCTCAAGTTGCTCTTGAATCTGAGATTCGTATGATGATGATGATGATGAT 575
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QY 421 TTGGAGTTTCAATTTGGAATCTGCTGCGGGTGTCTGTTGCTGATATAGAGATGAGCA 480
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Db 576 TTGGAGTTTCAATTTGGAATCTGCTGCGGGTGTCTGTTGCTGATATAGAGATGAGCA 635
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|
QY 481 GGAAGACTGAGTTTGTCTGAAAGCCCTTCTGTTATAGATATCAATTTGCTTATCGCT 540
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Db 636 GGAAGACTGAGTTTGTCTGAAAGCCCTTCTGTTATAGATATCAATTTGCTTATCGCT 695
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QY 541 TCAATAGCAGTTGTTTCTGCAAAACTCAGGGTAAATATTTTTCGACGTCGACATCA 600
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QY 601 AGTCTCCGTTTCTTCAAGATCTCCGCAATGAGCGGATGAGCCGAAAGGGAGGACATTTGG 660
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QY 661 AATTTACTGGGTTCACTGTTTATGCTCAACAGAAAGAAATTAATCAACCTTGTATAT 720
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QY 721 GGAATTTTGGTTCTTATTTTTCGTTCTTCTTCTTCTATCTGCTGGAAGAAAGTGCAT 780
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Db 876 GGAATTTTGGTTCTTATTTTTCGTTCTTCTTCTTCTATCTGCTGGAAGAAAGTGCAT 935
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QY 781 AAGAGTTTTCATCATATGCAAGATGCTCTGCTGGGAGCAATTAATTTGCAACATAT 840
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QY 841 GGCTATGAGACAAAACTCCCTTAACCTTGGCTGGGAAATTTGCTTCTGACGCTTTGCA 900
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QY 901 CTCCTTGGCAATTTCTTCTTTCGACTTCTGCGGCAATTTCTGCTCAGGTTTTCATTA 960
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Db 1056 CTCCTTGGCAATTTCTTCTTTCGACTTCTGCGGCAATTTCTGCTCAGGTTTTCATTA 1115
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QY 961 AAGATCAAGAAACAACCGCCGCAAAACAATTTGAGAAAGAAAGAAACCCAGTGCAC 1020
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Db 1116 AAGATCAAGAAACAACCGCCGCAAAACAATTTGAGAAAGAAAGAAACCCAGTGCAC 1175
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QY 1021 CTCATTCAGTGTGTGCGGTAGTTACGAGCTGATGAGAAATCTGTTTCAATTTGCAAC 1080
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Db 1176 CTCATTCAGTGTGTGCGGTAGTTACGAGCTGATGAGAAATCTGTTTCAATTTGCAAC 1235
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QY 1081 TGAAGCCACACTTGAAGGCTTTGACACCTGACGCTTACCAAGAAACAAGGGGAA 1140
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Db 1236 TGAAGCCACACTTGAAGGCTTTGACACCTGACGCTTACCAAGAAACAAGGGGAA 1279
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QY 1141 GCATCAAGAGATCAGAGGATTAATTTAGAGAGCAAGTGGGATGAGGAGGAGG 1200
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Db 1280 -----TCAGAGCTTAAGTTTAAAGAGCGAGTGGATGAGGAGGAGGAGG 1328
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QY 1201 CAGAGTATTAAGAGCGGACCAAGCTTCAGTATGAGTGAAGAGGATCCCAAGCAACGATC 1260
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Db 1329 CAAAGTAATTAAGAGCCGACAAAGCCTCAGTAGTGACAGAGAGTCCCAAGCACCGACATC 1388
Qy 1261 ACAGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGCTTGAGCTTCAACGACGACCCG 1320
Db 1389 ACAGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGCTTGAGCTTCAACGACGACCCG 1448
Qy 1321 TTCGGGCGCTCGCTGCGCCTCAAAAGTTCTCAGCCCAAAACCACTGATAGATGCTGAC 1380
Db 1449 TTCGGGCGCTCGCTGCGCCTCAAAAGTTCTCAGCCCAAAACCACTGATAGATGCTGAC 1508
Qy 1381 GCGCTTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1509 GCGCTTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1568
Qy 1441 GACCTGACCCCACTTAATAAATCTGTCATTCGAGCTATCAGAAATTAATAAATTCATG 1500
Db 1569 GACCTGACCCCACTTAATAAATCTGTCATTCGAGCTATCAGAAATTAATAAATTCATG 1628
Qy 1501 GCAGAAACGGAAGTTTAAAGAAACCTTACATGATGATGATGATGATGATGATGATGAT 1560
Db 1629 GCAGAAACGGAAGTTTAAAGAAACCTTACATGATGATGATGATGATGATGATGATG 1688
Qy 1561 TATTCGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1689 TATTCGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1748
Qy 1621 CAAATTCCTTGAGAAAGGCGAAATCACATCAGATGATGATGATGATGATGATGATGATG 1680
Db 1749 CAAATTCCTTGAGAAAGGCGAAATCACATCAGATGATGATGATGATGATGATGATGATG 1808
Qy 1681 GAAATGAGACCAAGACGATCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1809 GAAATGAGACCAAGACGATCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1868
Qy 1741 GTACAGTCCATGAAATCCAAAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 1869 GTACAGTCCATGAAATCCAAAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1928
Qy 1801 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTTCATTCAGATGCTGCTGCTGCTGCTGCTG 1860
Db 1929 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTTCATTCAGATGCTGCTGCTGCTGCTGCTG 1988
Qy 1861 CAGACATCTGACTATCAAAAGCCTGTGATAGCAAAAGATCTTTCGGGTTCCGACAAAC 1920
Db 1989 CAGACATCTGACTATCAAAAGCCTGTGATAGCAAAAGATCTTTCGGGTTCCGACAAAC 2048
Qy 1921 AGTGGCTGCTATCCAGATCACTAGTGGCAATCTCGAGAGGCGCTGAGTTCAATTCG 1980
Db 2049 AGTGGCTGCTATCCAGATCACTAGTGGCAATCTCGAGAGGCGCTGAGTTCAATTCG 2108
Qy 1981 AGGCCAAATGAGTTCAAGTCCCAAGCTTTCAGCGCTTACGCTTACATGACAGTCAA 2040
Db 2109 AGGCCAAATGAGTTCAAGTCCCAAGCTTTCAGCGCTTACGCTTACATGACAGTCAA 2168
Qy 2041 GCACACAGAGTCCCAATTAAGTCAAAAGCAGTGGCTCAGAGTGGACCCCAACCACT 2100
Db 2169 GCACACAGAGTCCCAATTAAGTCAAAAGCAGTGGCTCAGAGTGGACCCCAACCACT 2228
Qy 2101 GCAGAAACCAATTAATTCAGGCAACCAAGCAGAGGCGCCCAACCACTTACATGATCCACT 2160
Db 2229 GCAGAAACCAATTAATTCAGGCAACCAAGCAGAGGCGCCCAACCACTTACATGATCCACT 2288
Qy 2161 CCTCTCCAGCATCAAGCATCTGCCAGGCGCAAGAACTCTGACCCCTAACCTCGAGGC 2220
Db 2289 CCTCTCCAGCATCAAGCATCTGCCAGGCGCAAGAACTCTGACCCCTAACCTCGAGGC 2348
Qy 2221 TTACAGAAAGCATTTCTGACGTCACACCTGCTTGTTCCTCAAGGAAATGTTGAG 2280
Db 2349 TTACAGAAAGCATTTCTGACGTCACACCTGCTTGTTCCTCAAGGAAATGTTGAG 2408
Qy 2281 GTTGCACTGCAAAATCTCAAGGACGTTCTATAGGAAAGCTTTGACATGGAGAGA 2340

Db 2409 GTTGCACTGCAAAATCTCAAGGACGTTCTATAGGAAAGCTTTGACATGGAGAGA 2468
Qy 2341 GAAACTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2469 GAAACTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2528
Qy 2401 CAAACCTGATCAGGTGCAACCGAGAACTGAATATACAACTTTGAGGAGTGAATCACT 2460
Db 2529 CAAACCTGATCAGGTGCAACCGAGAACTGAATATACAACTTTGAGGAGTGAATCACT 2588
Qy 2461 GCGTCCAGAGGAGGCAAGATTTTACCCCAATGAGAGGAAATCCAAATGTTTAACT 2520
Db 2589 GCGTCCAGAGGAGGCAAGATTTTACCCCAATGAGAGGAAATCCAAATGTTTAACT 2648
Qy 2521 GATGAAGAGTGGGTCCGAGAGACAGAGACAGACACTTTTGATGCGCACCGAGCT 2580
Db 2649 GATGAAGAGTGGGTCCGAGAGACAGAGACAGACACTTTTGATGCGCACCGAGCT 2708
Qy 2581 GCCAGGAAAGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAG 2640
Db 2709 GCCAGGAAAGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAG 2768
Qy 2641 AGCATTTGTAAGGACGAGAAAGTACAGATGCGCTCAGCTGCTCATGTCAACTGAAA 2700
Db 2769 AGCATTTGTAAGGACGAGAAAGTACAGATGCGCTCAGCTGCTCATGTCAACTGAAA 2828
Qy 2701 TAACTTCTCAATTTCTTCCAGGATAGCAGTTCTTACGATATCATATCATTCATG 2760
Db 2829 TAACTTCTCAATTTCTTCCAGGATAGCAGTTCTTACGATATCATATCATTCATG 2888
Qy 2761 ACTATTTGAAAGCCCTTCTAATAAGTTGAATTCAGAAATCGGAGAAACATGAAAG 2820
Db 2889 ACTATTTGAAAGCCCTTCTAATAAGTTGAATTCAGAAATCGGAGAAACATGAAAG 2948
Qy 2821 CAGTTTAAAGCCGCTTACCTTTTAAATGCAAGAAAGCATGTTTAAAGGATGCTAAA 2880
Db 2949 CAGTTTAAAGCCGCTTACCTTTTAAATGCAAGAAAGCATGTTTAAAGGATGCTAAA 3008
Qy 2881 TTCCAAGGTGATGACATTAACCACTCATTTAGTATGATACCTTGAGTTAAAAAGCT 2940
Db 3009 TTCCAAGGTGATGACATTAACCACTCATTTAGTATGATACCTTGAGTTAAAAAGCT 3067
Qy 2941 GAGAAACCAAAACACAGCTTAATGCTATGGGTGATGATATGT 2983
Db 3068 GAGAAACCAAAACACAGCTTAATGCTATGGGTGATGATATGT 3111

RESULT 3
US-09-813-148-1
/ Sequence 1, Application US/09813148
/ Patent No. 6617131
/ GENERAL INFORMATION:
/ APPLICANT: STEINMEYER, Klaus
/ APPLICANT: LERCHER, Christel
/ APPLICANT: SCHERER, Constanze
/ APPLICANT: SEEBOW, Guido
/ APPLICANT: BUSCH, Andreas E.
/ TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
/ FILE REFERENCE: 38005-119
/ CURRENT APPLICATION NUMBER: US/09/813,148
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: DE 100 13 732.6
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/194,041
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-813-148-1

Query Match 93.0%; Score 2857.4; DB 4; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGAGCGGCATGAAAGATGTGAGTCCGGCCCGGGGCAAGGGTCTGCTGAACTCGGCAACC 60
DB GCGAGCGGCATGAAAGATGTGAGTCCGGCCCGGGGCAAGGGTCTGCTGAACTCGGCAACC 265
QY 61 GCGAGCGGCATGAAAGATGTGAGTCCGGCCCGGGGCAAGGGTCTGCTGAACTCGGCAACC 120
DB GCGAGCGGCATGAAAGATGTGAGTCCGGCCCGGGGCAAGGGTCTGCTGAACTCGGCAACC 325
QY 121 GGTGGCTGAGGAGAGAGCCGCGGGGCAAGAGGGGGCCGAGATGAGCCTGTGGGGAAAG 180
DB GGTGGCTGAGGAGAGAGCCGCGGGGCAAGAGGGGGCCGAGATGAGCCTGTGGGGAAAG 385
QY 181 CGGCTCTTTACACGAGTACGAGAGTCCCGGCGCAACTCAAGTACCGGGGGGTGACAG 240
DB CGGCTCTTTACACGAGTACGAGAGTCCCGGCGCAACTCAAGTACCGGGGGGTGACAG 445
QY 241 AACTACTGTACACGCTGCTGAGAGAGCCCGGGGCTGGGCGCTTCACTTCAACAGCTTTC 300
DB AACTACTGTACACGCTGCTGAGAGAGCCCGGGGCTGGGCGCTTCACTTCAACAGCTTTC 505
QY 301 GTTTTCTCCTTGTCTTTGGTGTGCTTGAATTTTGTACAGTGTCTTCAACATCCCTGAGAC 360
DB GTTTTCTCCTTGTCTTTGGTGTGCTTGAATTTTGTACAGTGTCTTCAACATCCCTGAGAC 565
QY 361 ACAAAATGCGCTCAAGTTCCTCTTGATCTGAGAGTGTGATGATGTGCTTGTGT 420
DB ACAAAATGCGCTCAAGTTCCTCTTGATCTGAGAGTGTGATGATGATGTGCTTGTGT 625
QY 421 TTGGAGTTCATCTTGGAAATCTGTGCTGCGGGTGTGCTGTGATGATGAGATGAGCA 480
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QY 481 GGAAGACTGAGTGTGCTGCAAAAGCCCTTGTGTTATGATACATTTGCTTATCGCT 540
DB GGAAGACTGAGTGTGCTGCAAAAGCCCTTGTGTTATGATACATTTGCTTATCGCT 745
QY 541 TCAATAGCAAGTGTCTTGTGCAAAAGCTCAGGGTAAATATTTTGTGCAAGTGTGCAAG 600
DB TCAATAGCAAGTGTCTTGTGCAAAAGCTCAGGGTAAATATTTTGTGCAAGTGTGCAAG 805
QY 601 AGTCTCCGTTCTTCAAGATCTTCCGATGTGCGATGAGTGAACGAAAGGGAGGCACTTGG 660
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QY 661 AAATTAAGGCTCAGTGTGTTATGCTCAGCAAGAAATTAATCAAGCTTGTGATCA 720
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QY 721 GGAATTTGGTCTTATTTTGTCTTCTTCTTCTATCTGATGAGAAAGATGCAAT 780
DB GGAATTTGGTCTTATTTTGTCTTCTTCTTCTTCTATCTGATGAGAAAGATGCAAT 985
QY 781 AAAGATTTTCTACATGAGATGCTCTGTGTTGGGCAATTAATTAATTAATTAATTA 840
DB AAAGATTTTCTACATGAGATGCTCTGTGTTGGGCAATTAATTAATTAATTAATTA 1045
QY 841 GGGTATGAGAGAAAAGTCCCTTAAGCTTGGCTGGGAAAGATTTGCTTCTGAGGCTTGA 900
DB GGGTATGAGAGAAAAGTCCCTTAAGCTTGGCTGGGAAAGATTTGCTTCTGAGGCTTGA 1105
QY 901 CTCCTTGGCATTTCTTTCTTTGCACTTCTGCGGCAATTTCTGAGTCTTGTGATTA 960
DB CTCCTTGGCATTTCTTTCTTTGCACTTCTGCGGCAATTTCTGAGTCTTGTGATTA 1165
QY 961 AAAGTACAGAAACAACCGCCGAGAAACATTTGAGAAAAGAAAGAAACCAAGCTGCAAC 1020
DB AAAGTACAGAAACAACCGCCGAGAAACATTTGAGAAAAGAAAGAAACCAAGCTGCAAC 1225

QY 1021 CTCATTCAAGTGTGTTGGCGTATGACGAGCTGATGAGAAAATCTGTTCCATTGCAACC 1080
DB CTCATTCAAGTGTGTTGGCGTATGACGAGCTGATGAGAAAATCTGTTCCATTGCAACC 1285
QY 1081 TGGAGCCCACTTTGAAAGCCTTTGCAACCTGACGCTTCAACAAAGAAACAAGGGGAA 1140
DB TGGAGCCCACTTTGAAAGCCTTTGCAACCTGACGCTTCAACAAAGAAACAAGGGGAA 1345
QY 1141 GCATCAAGAGTTCAGAAAGTTTAAGTAAAGAGAGTCCGATGGCTAGGCCCAAGGGG 1200
DB GCATCAAGAGTTCAGAAAGTTTAAGTAAAGAGAGTCCGATGGCTAGGCCCAAGGGG 1405
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QY 1321 TTCCGGCCTCGCTGCGCTCAAAAGTTTCAAGCCAAACAGTGTATGATGCTGACACA 1380
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QY 1381 GCGCTTGGCACTGATGATATATGATGAAAAAGATGCGAGTGTATCACTGAGAA 1440
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QY 1441 GACCTAACCCCACTTAACCTGTCAATTCAGCTATCAAGATTAAGAAATTTCACTGT 1500
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QY 1801 AAAGGCTGCTCAGAGCCCTGCTTGTGCTTCAATTCAGTTCACCTTTGAATGTGA 1860
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DB CAGACATCTGATTAACAAAGCCCTGTGATGATCAAGATCTTTGGGTTCCGACAAAAC 2125
QY 1921 AGTGGCTGCTTATCAAGATCACTAGTGCACATCTCAGAGAGCCTGAGTTCAATTCG 1980
DB AGTGGCTGCTTATCAAGATCACTAGTGCACATCTCAGAGAGCCTGAGTTCAATTCG 2185
QY 1981 ACGCCAATGAGTTAGTCCGACACTTTCTACGCGCTTAAAGCTTATGATGACAGTCAA 2040
DB ACGCCAATGAGTTAGTCCGACACTTTCTACGCGCTTAAAGCTTATGATGACAGTCAA 2245
QY 2041 GGAACACAGGTCCCAATTAAGTCAAGAGATGCTCAGAGTGTGAGCCAGCAACCAAT 2100
DB GGAACACAGGTCCCAATTAAGTCAAGAGATGCTCAGAGTGTGAGCCAGCAACCAAT 2305
QY 2101 GCAAAACAAATTAATGAGCAACCAAGCAGAGCCCAACCACTTACAGATCCACCT 2160

Db	2306	GCAAAACCAATTAATACGGACCCACAGCAGCAGCCCAACACTTTACAGATCCACCT	2365
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Db	2366	CCTGTCCAGGCATCAAGCATCTGTGCGCGAGGCGAGAACTTGTGCACCTTAACCTTGCAGGC	2425
Qy	2221	TTACAGGAAAGCATTTTCTGAGTCAACCACTTGTCTTGTGCTCCAGGAAATGTTTCAG	2280
Db	2426	TTACAGGAAAGCATTTTCTGAGTCAACCACTTGTCTTGTGCTCCAGGAAATGTTTCAG	2485
Qy	2281	GTTGCACAGTCAAACTCAGCCAGGACCGTTCTATAGAGAAAGCTTTGACATGGAGGA	2340
Db	2486	GTTGCACAGTCAAACTCAGCCAGGACCGTTCTATAGAGAAAGCTTTGACATGGAGGA	2545
Qy	2341	GAACCTCTGTTGTCTGTCTGTCTCCATGTGTGCGAGAGACTTGGGCAATCTTGTCTGTG	2400
Db	2546	GAACCTCTGTTGTCTGTCTGTCTCCATGTGTGCGAGAGACTTGGGCAATCTTGTCTGTG	2605
Qy	2401	CAAAACCTGATCAGTGCAGCCAGGAACTGAATATACAATTTTCAGGAGTGAAGTCAAGT	2460
Db	2606	CAAAACCTGATCAGTGCAGCCAGGAACTGAATATACAATTTTCAGGAGTGAAGTCAAGT	2665
Qy	2461	GGCTCCAGGACAGCAGATTTTATCCCAATGAGAGGAATCCAAATGTGTTATTAAT	2520
Db	2666	GGCTCCAGGACAGCAGATTTTATCCCAATGAGAGGAATCCAAATGTGTTATTAAT	2725
Qy	2521	GATGAGAAGTGTGGTCCCGAAGAGACAGACACTTTTGAATGCCAGCCAGCCT	2580
Db	2726	GATGAGAAGTGTGGTCCCGAAGAGACAGACACTTTTGAATGCCAGCCAGCCT	2785
Qy	2581	GCCAGGGAAGCTGCTTTGGCATCAGACTCTCTAAGACTGAAGGTCAAGATCTTCAG	2640
Db	2786	GCCAGGGAAGCTGCTTTGGCATCAGACTCTCTAAGACTGAAGGTCAAGATCTTCAG	2845
Qy	2641	AGCATTTGTAAAGCGAGGAGAAAGTACAAATGCGCTCAGCTTGCATAGTCAAACTGAAA	2700
Db	2846	AGCATTTGTAAAGCGAGGAGAAAGTACAAATGCGCTCAGCTTGCATAGTCAAACTGAAA	2905
Qy	2701	TAAGTTCTTCAATTTCTTCCAGGACTAGAGTTCTTAAAGCATACATATCATTTGCATGA	2760
Db	2906	TAAGTTCTTCAATTTCTTCCAGGACTAGAGTTCTTAAAGCATACATATCATTTGCATGA	2965
Qy	2761	ACTATTTGAAAGCCCTTCTAAAAAGTTGAAATTGCAAGATCGGAGAGAAATGAAAGG	2820
Db	2966	ACTATTTGAAAGCCCTTCTAAAAAGTTGAAATTGCAAGATCGGAGAGAAATGAAAGG	3025
Qy	2821	CAGTTTATTAAGCCGTTACCTTTTATTTGATGAAATGCAATGCTTTTAGG	2869
Db	3026	CAGTTTATTAAGCCGTTACCTTTTATTTGATGAAATGCAATGCTTTTAGG	3074

[illegible]

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DB 1057 AAAGTACAAGAACACACCGCAGAAAACCTTTGAGAAAAAGAGAACCCAGCTGCCAAC 1116
QY 1021 CTCATTGAGTGTGTGGCGGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACC 1080
DB 1117 CTCATTGAGTGTGTGGCGGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACC 1176
QY 1081 TGGAAAGCCACATTGAAAGGCTTGACACCTGACGCCCTTACCAAGAAAGAACAGGGGAA 1140
DB 1177 TGGAAAGCCACATTGAAAGGCTTGACACCTGACGCCCTTACCAAGAAAGAACAGGGGAA 1220
QY 1141 GCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGGAGTGGCAGATGGCTAGCCCGAGGGGC 1200
DB 1221 -----TCAGAAAGCTAAGTTTAAAGAGGAGTGGCAGATGGCTAGCCCGAGGGGC 1269
QY 1201 CAGAGTATTTAAGAGCCGACAGGCTCAGTAGTGAAGAGGTCCCAAGCAGCAGATC 1260
DB 1270 CAGAGTATTTAAGAGCCGACAGGCTCAGTAGTGAAGAGGTCCCAAGCAGCAGATC 1329
QY 1261 ACAGCCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGC 1320
DB 1330 ACAGCCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGC 1389
QY 1321 TTCGGGCGCTCGCTGCGCTCAAAAAGTTCTCAGCCAAAACAGTAGATAGTGCAGACA 1380
DB 1390 TTCGGGCGCTCGCTGCGCTCAAAAAGTTCTCAGCCAAAACAGTAGATAGTGCAGACA 1449
QY 1381 GCCCTTGAGCCTGATGATGATATGATGAAAAAGATGCCAGTGTATGATGAGTGA 1440
DB 1450 GCCCTTGAGCCTGATGATGATATGATGAAAAAGATGCCAGTGTATGATGAGTGA 1509
QY 1441 GACCTCAACCCACCTTAAACTGTCTATTCGAGCTATCGAATTATGAAATTTTCACTT 1500
DB 1510 GACCTCAACCCACCTTAAACTGTCTATTCGAGCTATCGAATTATGAAATTTTCACTT 1569
QY 1501 GCAAAAACGGAAGTTTAAAGAAACCTTACGTCAATGATGATGAAAAAGTGCATTGAA 1560
DB 1570 GCAAAAACGGAAGTTTAAAGAAACCTTACGTCAATGATGATGAAAAAGTGCATTGAA 1629
QY 1561 TATTTGCTGTGATCATGAGCATGTTGTGATGAAATTTAAAGCCTTCAACAGCTGTGAT 1620
DB 1630 TATTTGCTGTGATCATGAGCATGTTGTGATGAAATTTAAAGCCTTCAACAGCTGTGAT 1689
QY 1621 CAAATTTCTGAAAAAGGCGAAATCATCATGATTAAGAGAGCCGAGAGAAAAATTAACGA 1680
DB 1690 CAAATTTCTGAAAAAGGCGAAATCATCATGATTAAGAGAGCCGAGAGAAAAATTAACGA 1749
QY 1681 GAACATGAGACACAGACGATCTCAGATGCTGGTCCGGTGGTCAAGGTTGAAAAACAG 1740
DB 1750 GAACATGAGACACAGACGATCTCAGATGCTGGTCCGGTGGTCAAGGTTGAAAAACAG 1809
QY 1741 GTACAGTCCATAGATTCAGAGTGAAGTGCCTTCTAGACATCTTATCAACAGTCTCTCG 1800
DB 1810 GTACAGTCCATAGATTCAGAGTGAAGTGCCTTCTAGACATCTTATCAACAGTCTCTCG 1869
QY 1801 AAAGGCTGCTGACAGCCCTGCTGCTTGGCTTCAATTCAGTTCCCACTTTTGAATGAA 1860
DB 1870 AAAGGCTGCTGACAGCCCTGCTGCTTGGCTTCAATTCAGTTCCCACTTTTGAATGAA 1929
QY 1861 CAGACATCTGATCATCAAAAGCCCTGAGATGAGCAAAAGATCTTTCGGGTTCCGACAAAAC 1920
DB 1930 CAGACATCTGATCATCAAAAGCCCTGAGATGAGCAAAAGATCTTTCGGGTTCCGACAAAAC 1989
QY 1921 AGTGGCTGCTTATTCAGATCAACTAGTGCAGACATCTCGAGAGCCCTGCACTTCTG 1980
DB 1990 AGTGGCTGCTTATTCAGATCAACTAGTGCAGACATCTCGAGAGCCCTGCACTTCTG 2049
QY 1981 AGCCCAAAAGATTTCACTGCTCCAGACTTTTACGCGCTTAGCCCTACTATGACAGTCA 2040
DB 2050 AGCCCAAAAGATTTCACTGCTCCAGACTTTTACGCGCTTAGCCCTACTATGACAGTCA 2109

QY 2041 GCAACACAGGTGCAATTAAGTCAAGAGATGGCTCAGAGTGGCAGCCACCAACACCAT 2100
DB 2110 GCAACACAGGTGCAATTAAGTCAAGAGATGGCTCAGAGTGGCAGCCACCAACACCAT 2169
QY 2101 GCAACCAAAATAAATACGGGACCCCAAGCAGACGCCCAACCAACTTTACAGATCCACCT 2160
DB 2170 GCAACCAAAATAAATACGGGACCCCAAGCAGACGCCCAACCAACTTTACAGATCCACCT 2229
QY 2161 CCTCTCCAGCCATCAAGATCTGCCAGGCCGAAACTCTGACCTTAACCTTGCAGGC 2220
DB 2230 CCTCTCCAGCCATCAAGATCTGCCAGGCCGAAACTCTGACCTTAACCTTGCAGGC 2289
QY 2221 TTACAGAAAAGCATTTCTGACGTCACACCTGCTGTTGCTCCCAAGGAAAAATGTTCA 2280
DB 2290 TTACAGAAAAGCATTTCTGACGTCACACCTGCTGTTGCTCCCAAGGAAAAATGTTCA 2349
QY 2281 GTTGCAAGTCAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGA 2340
DB 2350 GTTGCAAGTCAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGA 2409
QY 2341 GAAACTGTGTGTCTGTCTGTCCATGTGTCCGAAAGACTTTGGGCAAACTTTGTCTGTG 2400
DB 2410 GAAACTGTGTGTCTGTCTGTCCATGTGTCCGAAAGACTTTGGGCAAACTTTGTCTGTG 2469
QY 2401 CAAAACCTGATCAGTGCAGCCGAGAACTGAATATCAACTTTCAAGGAGTGAAGT 2460
DB 2470 CAAAACCTGATCAGTGCAGCCGAGAACTGAATATCAACTTTCAAGGAGTGAAGT 2529
QY 2461 GGCTCCAGAGGACCCCAAGATTTTAAACCCCAATGGAGGAAATCCAAATTTGTTATTA 2520
DB 2530 GGCTCCAGAGGACCCCAAGATTTTAAACCCCAATGGAGGAAATCCAAATTTGTTATTA 2589
QY 2521 GATGAAGAGTGGGTCCCAAGAGACAGACAGACACTTTTGAATGCCGACCGACCT 2580
DB 2590 GATGAAGAGTGGGTCCCAAGAGACAGACAGACACTTTTGAATGCCGACCGACCT 2649
QY 2581 GCCAGGAGAGTGGCTTTGATCAGACTCTTGAAGAGTGAAGGTCAGATCATCTGAG 2640
DB 2650 GCCAGGAGAGTGGCTTTGATCAGACTCTTGAAGAGTGAAGGTCAGATCATCTGAG 2709
QY 2641 AGCATTTGTAAGGCAAGAGAAAGTACAGATGCCCTTCAGCTTGCATATCAAACTGAA 2700
DB 2710 AGCATTTGTAAGGCAAGAGAAAGTACAGATGCCCTTCAGCTTGCATATCAAACTGAA 2769
QY 2701 TAA 2703
DB 2770 TAA 2772

RESULT 5
US-09-949-016-1823
/ Sequence 1823, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 1823
/ LENGTH: 2196
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-1823

Query Match 16.9%; Score 518; DB 4; Length 2196;
 Best Local Similarity 60.1%; Pred. No. 5e-145;
 Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

226 TACCGCGGGGTGACAACTACCTGTACAACTGTCTGGAAGAGACCCCGGGCTGGGGCTTC 285
 181 TACCGCGGGGTGACAACTACCTGTACAACTGTCTGGAAGAGAGCGCCCGGGCTGGGGCTTC 240
 286 ATCTACCAAGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 345
 241 GCTTACCAAGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 300
 346 ACCATCCCTGAGACACAAATTTGGCTCAAGTTGCTCTTGAATCTGTGAGTTGCTGATG 405
 301 ACTATCCAGAGACACAGGAACTTGGCAACGAGTCTCTCATCTTGAATTTGCGATG 360
 406 ATTTGCTCTTGTGTTGAGTTGATTCATTCATTCGAAATCTGTCTGGGGTGTCTGTTCGA 465
 361 ATCTGCTTCTGCTTGTGAGTTGATTCATTCGAAATCTGTCTGGGGTGTCTGTTCGA 420
 466 TATAGAGATGGCAAGAACTGAGTTGCTGCAAGAGCCCTTCTGTATATGATAC 525
 421 TACCGAGATGGCAAGAGTCTGCTTCTGCTTCTGCAAGAGCCCTTCTGTATATGATAC 480
 526 ATTTGCTTATGCTTCAATAGCAGTTGTTTCTGCAAAATCTGAGGTAATATTTTTC 585
 481 ATCTGCTTCTGCTTGTGAGTTGATTCATTCGAAATCTGTCTGGGGTGTCTGTTCGA 540
 586 AGCTGCTGCACTGAGAGTCTGCTTCTGCAAGATCTCTGCAATGTTGCTGCAATGAGCA 645
 541 AGCTGCTGCTGCTGCAAGTCTGCTTCTGCAAGATCTCTGCAATGTTGCTGCAATGAGCA 600
 646 AGGAGGAGCACTTGAATTTACTGAGTTGCTGCAAGATCTCTGCAATGTTGCTGCAATGAGCA 705
 601 CGCGGGGAGCACTGAGAGTCTGCTTCTGCAAGATCTCTGCAATGTTGCTGCAATGAGCA 660
 706 ACAGCTTGTATGAGATTTTGTGTTCTTATTTTCTGCTTCTGCTTCTATCTGCTG 765
 661 ACCGCTGCTGATCATCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 766 GAAAGAGATGCAATTAAGATTTTCTAATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCT 825
 721 GAAAGAGATGCAATTAAGATTTTCTAATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCT 780
 826 ACATTTGACAACTATTTGCTATGAGAGCAAAATCTCCCTAATCTGCTGAGAAATGCTT 885
 781 ACATTTGACAACTATTTGCTATGAGAGCAAAATCTCCCTAATCTGCTGAGAAATGCTT 840
 886 TCTGAGGCTTTGCACTCTTGGCAATTTCTTTTCTTGTGCACTTCTGCTGCTGCTGCTGCT 945
 841 GCTGCTGCTGCTGCTTCTTCTGCTGCTGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCT 900
 946 TCAGGTTTGGCAATTAAGATTAAGAGCAAAATCTCCCTAATCTGCTGAGAAATGCTT 1005
 901 TCAGGTTTGGCAATTAAGATTAAGAGCAAAATCTCCCTAATCTGCTGAGAAATGCTT 960
 1006 AACCCAGCTGCAAACTTCAATGCTGTTTGGCTGATTTAGCACTGAGTGAATCT 1065
 961 ATGCGGGAGCAAACTTCAATGCTGTTTGGCTGATTTAGCACTGAGTGAATCT 1020
 1066 GTTTCATTTGCACTGAGAGCACTTGAAGGCTTGTGCACTGCTGAGC----- 1116
 1021 GCTTACCTACAGCCACTGTGTAATCTATGACAGTATCTCTCCATCTTTCAGAGAGCTG 1080
 1117 CTTACCAAGAAAGAAAG 1161
 1081 GCTCTCTTGTGTTGAGACGTGCAAGGAGCCGCAATGAGGAGCTTACGAGGCTTGAAGTGT 1140
 1162 ----- 1161
 1141 CGGCGGGGCGCGGTACCGAGCGAGACCTCTCCGTTACCCGCGCGTGTGCACTGCTGCA 1200

1162 -----AGTTTAAGAGCGA 1176
 1201 CGGCGGGAGACCTCTTCTGCTGCTGAGGAAAGACCGAGATGGCATCAAAAGACGCG 1260
 1177 GTGCGCATGCTAGGCGCCAGAGGCGCAG-----CTATTAAGAGCGCAAGGCTCAGTA 1230
 1261 ATCCGATGAGGAGCTCCAGAGGCGAGAGGCTCTTCCAGAGAGACATCTGACCTCCA 1320
 1231 GGTGACAGAGGTTCCCAAGACCGCATCAAGCCGAGG---GCACTCCCAAGAGT 1287
 1321 ACAATGCCACCTCCCAAGAGAGGAGAGAGGAGTGAAGGACACAGGCCCAAGAGT 1380
 1288 CAGAAAGCTGAGAGCTTCAAGACCGAAACCGCTTCCGAGCTCTGCTGAGCTCAAAAGT 1347
 1381 CAAAAGACTGAGAGCTTCAAGTACCGAACCGCTTCCGAGATCTCTAGAGCTC----- 1434
 1348 TCTCAGCAAAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
 1435 -----AAACCCCGACCTCTGCTGAGAGATGCC---CTTCAAGAGAGTACAGAG 1482
 1408 GAAAGAGATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467
 1483 GAGAGAGCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542
 1468 ATTGAGCTATCAGATTTATGAAATTTTATGTTGCAAAACGAGATTTAAGAAACRTTA 1527
 1543 ATCCGCTCATCAGATTTCTCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1602
 1528 GCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
 1603 CAGCCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662
 1588 TGTAGATTTAAAGCTTCAACAGTGTGATCAATTTCTTGAAGAGGCG---AAATC 1644
 1663 GCGCGGATCAAGAGCTGCTCAAACTCGGTTGAGCAAAATTTGTTGGTTCGCGGCGCGGAGC 1722
 1645 ACATGATTAAGAGAGCGGAGAGAAATTAACAGAGAAATGAGAACACAGACATCTC 1704
 1723 AGAAAGGCGCGGAG 1782
 1705 AGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1764
 1783 AGCATGATGAGAGCGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1842
 1765 GACTGCTTACTAGACATCTATCAAGGTCCTTGGAAAGGCTGCTGCTGCTGCTGCTGCTGCT 1824
 1843 GACTGCTGTTGGGCTTCTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1896
 1825 TTGCTTACTTCAATTTCCACCTTTTGAATGTAAGACAGACATCTGAATTAAGAGCTT 1884
 1897 CTGGGCGCGGAG 1956
 1885 GTGATAGCAAAAGATCTTTCGGGTTCCGACAAA 1918
 1957 GTGACACAGAGACATCTCCGTCTCCGACAGA 1990

RESULT 6
 US-09-492-361-1
 ; Sequence 1, Application us/09492361
 ; Patent No. 6794161
 ; GENERAL INFORMATION:
 ; APPLICANT: JENTISCH, Thomas J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
 ; TITLE OF INVENTION: POTASSIUM CHANNELS
 ; FILE REFERENCE: 2815-127P
 ; CURRENT APPLICATION NUMBER: US/09/492,361
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2335
 ; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2335)
NAME/KEY: CDS
LOCATION: (83)..(2170)
US-09-492-361-1

Query Match 16.9%; Score 518; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 5.3e-15;
Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

226 TACCGCGGGTGAGAACTACCTGACAGCTGTGAGAGACCCCGGCTGGGCTTC 285
Db TACCGCGGGCTGAGAACTGGGTCTACAGTGTGAGAGGCGCCCGGCTGGGCTTC 379
286 ATCTACAGCGCTTTCCTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 345
Db GTCTACACGCTCTCAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
346 ACCATCCCTGAGGACAAATTTGGCTCAAGTTGGCTCTGATCCCTGGAGTTGCTGATG 405
Db ACTATCCAGAGACCAAGAACTTGCACAGAGTCTCTCAATCTTGGAAATCTGATG 499
406 ATTGCTGCTTTGGTTGAGTTCAATCATTCGAATCTGCTGCGGGTGTCTGTTGCTGA 465
Db ATGCTGTTTGGCTTGGAGTACATGCTCGGGTCTGCTCGCGGATGCTCTGCTGCGG 559
466 TATAGAGATGCGAAGAGACTGAGTTGCTCGAAAGCCCTTCTGCTTATATATACC 525
Db TACCGAGATGCGAGGGTCTGCTTCCGCTTTCAGAAAGCCCTTCTGCTATCATGACTTC 619
526 ATGCTCTTATGCTTCAATAGAGTTGTTCTGCAAAAATCTAGGTAATATTTTTCG 585
Db ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
586 ACCTGCTGCACTGAGAGTCTCCGTTTCTACAGATCCTCCGATGGTGCATGAGACGA 645
Db ACCTCGCGCTGGCGAGCATGCGCTTCTGCAATCTGCGATGATGATGCGCATGAGACCG 739
646 AGGGAGGCACTTGGAAATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
Db CGCGGGGCGGACCTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
706 ACAGCTTGGTACATAGATTTTGGTTCTATTTTCTGCTTCTGCTGCTGCTGCTGCTGCTG 765
Db ACCGCTGCTGATCCGAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
766 GAAAGAGATGCAATTAAGATTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTG 825
Db GAAAGAGATGCAATTAAGATTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTG 919
826 ACATTAACAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
Db ACATTAACAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
920 ACATTAACAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 945
886 TCTGCAAGCTTGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
Db GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
946 TCAAGTTTTCATTAATAAGTACAAAGAACCAACCGGACAGAAACCTTGAAGAAAGAG 1005
Db TCGGGCTTTGGCTTAAGGTCAGAGAGCAACCGGACAGAAAGCTTGAAGAAAGAGAG 1099
1006 AACCCAGCTGCAACTCATTCAGTGTGTTGGCTGATGTTACGACAGTATGAAATCT 1065
Db ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159
1066 GTTTCATGCAACTGGAAGCACTTGAAGGCTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTG 1116
Db GCTTACCTGACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1219
1117 CCTACCAAGAAAGAACAGAGGAGATCAGAGCTGCAAGCTA----- 1161

1220 GCCCTCTGTTTATGACACGTCGCAACGGCGCCGCAATGGGGGCTTACGGCCCTGAGAGTG 1279
1162 ----- 1161
1280 CGGCGGGCGCGGTACCCGACGAGAGACCTCCGTTACCCGCGCTTGCCACTGCGCAC 1339
1162 -----AGTTTAAGAGCGA 1176
1340 CGGCGGGCGACACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1399
1177 GTGCGCATGCTGACCCGAGGCGAGCA-----GATTATAGAGCCGACAGGCTCAGTA 1230
1400 ATCCGATGAGGAGCTGCTCCAGCGCGGAGCGGGTCTTCCAGAGAGAGAGTGGACCTCCA 1459
1231 GGTGACAGAGAGTCCCAAGACCGACATCACAGCGGAGG--GAGTCCCAAGAAAGTG 1287
1460 ACAATGCCACCTCCCAAGACGAGAGAGAGTGGAGAGGCGACAGCCCAAGAGTG 1519
1288 CAGAAAGCTGAGGCTTCAACGACCGGACCGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTG 1347
1520 CAAAGAGCTGAGGCTTCAATGACCGACCGCTTCCGCGCATCTTGAAGCTC----- 1573
1348 TCTCAGCCAAACCAAGTGAATGATGCTGACACAGCCCTTGGCACTGATGATATATGAT 1407
1574 -----AAACCCCGGACCTCTGCTGAGATGCCC-----CTCAGAGAGAGTACAGAG 1621
1408 GAAAGAGATGCGAGTGTATGATATGATGAGAGAGCTCACCCACCACTTAAACTGCTC 1467
1622 GAGAAAGCTTACAGAGTGTGAGCTCACAGTGTGAGAGATCATGCTGCTGTAAGACAGTC 1681
1468 ATTGAGCTATCAGAAATTAATGAAATTTCAATTTTGAAGAGAGTGAAGAAATRTA 1527
1682 ATCCGCTCATCAGAAATTTCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
1528 CGTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1587
1742 CGACGCTGACAGTGTGAGAGAGCTGATGAGAGAGTACTGAGAGAGCCACTGAGACATGCTG 1801
1588 TGTGAAATTAAGAGCTTCAACAGCTGTTGATCAAAATTTCTGGAAGAGGCG--AAATC 1644
1802 GGCCTGATCAAGAGCTGCAAACTCGGCTGAGACCAAAATTTGCTGCTGCTGCTGCTGCTG 1861
1645 ACATCAATTAAGAGAGCGGAGAGAAATAACAGCAAGATGAGACCAAGACGATCTC 1704
1862 AGAAGGCGCGGAGAGAGGCGACAAAGGCGCTTCCAGCGAGGCTGTGATGAAATC 1921
1705 AGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1764
1922 AGCATGATGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
1765 GACTGCTATCAAGATCTATCAAGAGTCTTTCGGAAGAGGCTGCTGCTGCTGCTGCTGCT 1824
1982 GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2035
1825 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1884
2036 CTGAGGCGCTGCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2095
1885 GTGATAGCAAGATCTTTCGAGTTCCGACAAA 1918
2096 GTGACACAGAGACATCTCGCTCCGACAGA 2129

RESULT 7
US-09-177-650-88
; Sequence 88, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KNO2 AND KNO3 - POTASSIUM CHANNEL GENES WHICH ARE

Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blonar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoef, Valentin K.
APPLICANT: Leveque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Men-Pin
TITLE OF INVENTION: KClO₄ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 22
LENGTH: 2169
TYPE: DNA
ORGANISM: mouse
US-09-105-058C-22

Query Match 16.7%; Score 511.6; DB 3; Length 2169;
Best Local Similarity 58.2%; Pired. No. 4.3e-143;
Matches 1044; Conservative 0; Mismatches 669; Indels 81; Gaps 5;

QY 73 GGGCTGCTACTGCTGGGCAACCCCGGCGCCACGCTTGCTGGCGCGCGGCTGAGG 132
DB 67 GGGCTGCTGGGGCTGGGACCCCGGCGCCGCGCTTGAAGCAAGCCGCGGCGGCGG 126
QY 133 GAGAGCCGCGCGGGGCAAGCGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTTAC 192
DB 127 GCGGGCTCGAGGCGCCCAAGCGCGGCGGCTTTGAGCAAGCCGCGGCGGCGGCGG 186
QY 193 ACGAGTACCGGAGCTGCGCGCGCAACCTCAAGTACCGCGGCGGCGGCACTACTGAC 252
DB 187 GAGCGCGGGAAGCGCCGGAAGCGCAAGCCTTCAAGCAAGCTGCAATTTCTCTAC 246
QY 253 AAGCTGCTGAGAGAGACCCCGCGGCTGGGCTTCACTCAACGCTTCTGTTTCTCTT 312
DB 247 AAGCTCTAGAGGCGCGCGCGGCTGGGCTTCACTCAACGCTTCTGTTTCTTAA 306
QY 313 GCTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 372
DB 307 GCTTTCTCTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 366
QY 373 TCAAGTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 432
DB 367 GAGGGGCGCTCAATCTTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 426
QY 433 ATTGAAATCTGCTGCGGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 492
DB 427 GTGAGATCTGCGGCTGAGGCTGCTGTTGCGGTTATCGAGGCTGAGGCGCAAG 486
QY 493 TTTGCTCGAAGCGCTTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 552
DB 487 TTTGCGAAGAGCGTTCTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 546
QY 553 GTTTCGCAAAAAGTGAATATTTTTCAGCGTGTGCACTGAGAGTCTCGTTTC 612
DB 547 CTGGCTGCTGTTCCAGGCAATGCTTTGCAATCTGCGTTGGAGCTTGGCGTTTC 606
QY 613 CTACAGATCTCCGATGCTGCGATGAGCGAAGGGGAGCACTTGAATTAATCTGGGT 672
DB 607 TTCCAATCTTGGGATGATCGATGAGCGGAGGGGAGCACTTGAAGCTCTTGGGA 666
QY 673 TCAGGTTTATGCTACAGAGGAATTAATCAAGCTTGTGATCAATGATTTTGGTT 732
DB 667 TCGGTATCTACGCTACAGAGAGAGCTGTGATCTGCTGATGATTTGCTTCTGCTGC 726
QY 733 CTATTTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 792

DB 727 CTATCTCGGCTCATTTCTGTGTACTTTGAGAAAAGGATGAGATGACACTTTGAC 786
QY 793 ACATATGAGATGCTCTGTGTGGGCAATTTATGATGACAATTTGCTATGAGAC 852
DB 787 ACCTAGCAGATGCTCTGTGTGGGCTGTGATCTACTGACATGACATTTGGCTAGGGAGC 846
QY 853 AAAAATCCCTTAATCTGTGGGAAAGTTGTTTCTGAGGCTTGTGACTCTTGGCATT 912
DB 847 AAGTACCTCAAGCTGGAACGGAGGCTGTGGAGGACCTTTTACCTCATTTGGTGTTC 906
QY 913 TCTTTTCTGCACTTCTGCGGCAATTTGCTGAGTTTGTGATTAAGTACAGAA 972
DB 907 TCGTTCTTGTCTTCTGCTGCTGCAATTTTGGGATCGGCTTTGCTTGAAGTCCAAAGG 966
QY 973 CAACACCGCAGAAACATTTGAGAAAAGAGAACCCAGCTGCAACTCATTTGAGGT 1032
DB 967 CAGCATGGCAAAAACATTTGAGAAAGCGGCAACCTTGGGAGGTGTGATCCAGTCT 1026
QY 1033 GTTTCGCTAGTTTACGACGATGAGAAAT----- 1063
DB 1027 GCTGAGATTTCTATGCTAATCCTTCAGGACCGACCTGCACTTCAAGGAGTAC 1086
QY 1064 -----CTGTTTCATTTGCACTTGAAGCCCACTTGAAGCCTTGCAC 1107
DB 1087 TACGAGCGGACAGTCACTGTCCCATGTACAGACTATCCACTTGAACAGCTGAG 1146
QY 1108 ACCTGAGCCCTACAGAG-----AAGACAGGGGAA 1140
DB 1147 CTGCTGAGAAATCTCAAGAGCAATCTGAGCTCACCTTCAAGAGAGCAGACGAGAG 1206
QY 1141 GCATCAAGAGCTCAGAACTAAGTTTAAAGAGCGAG--TCCGATGCTAGCCCGAG 1197
DB 1207 CCATCAAGAGCTCAGAACTAAGTTTAAAGAGCTTGAAGATCTTCTCAAGCCCGGAGCAG 1266
QY 1198 GGCAGAGTATTAAGAGCCGAGAGCTCAGTATGAGAGAGTCCCAAGACCGAG 1257
DB 1267 GCTGCCAAGGAAAGGGGCTCCCGAGCCGAGAGGCTCCGCGGCTCCCGAGTGGAT 1326
QY 1258 ATCAAGCGGAGAGGAGTCCCAAGAGTCAAGAGAGTGGAGCTTCAAGAGCGAAGC 1317
DB 1327 CAGAGCTTGAAGAGAGCCGAGAGAGTGGAGGCTTGGTGAAGCTGAGC 1386
QY 1318 CGCTTCGCGCCCTGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATGCTGAC 1377
DB 1387 CGCAGCGCAGAGCTTCCGATCAAGGCTGCTGATCCCGGCAATTCAGAGAGAAC 1446
QY 1378 ACAGCCCTTGGCACTGATGATGATATGATGAAAAAGATGCAAGTGTATCAAGT 1437
DB 1447 C---TCCCTGGGAGAGACATGTAAGAGCAACAAGAGCTGTAAGGAGTTGTGACT 1503
QY 1438 GAAAGCTTCAACCCCTGAGCTTCAAGAGTGTGATGAGAGTGTGATGAGGTTCTTG 1497
DB 1504 GAAAGCTTCAACCCCTGAGCTTCAAGAGTGTGATGAGAGTGTGATGAGGTTCTTG 1563
QY 1498 GTTGAAGAGAGGATTAAGAAACRTTACGTCATGATGATGATGATGATGATGATGAT 1557
DB 1564 GTATCTAAGCGAAAGTTCAAGAGAGTCTGCGCCCATGATGATGATGATGATGATGAT 1623
QY 1558 CAATATTTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1617
DB 1624 CAGTACTGGCTGAGACCTTGAATGTTGTCCGATCAAGAGCTGAGTCAAGAGT 1683
QY 1618 GATCAATTTCTTGAAGAGGCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1677
DB 1684 GACCAAGATTTGGGGGCGGCGCCCAATTAAGAGATTAAGAGATTAAGAGATTAAGAG 1740
QY 1678 GCAGAAATGAGACCAAGATCTCAGTATGCTCGGCTGGGAGTGTGAGTGAAGAA 1737
DB 1741 GCGGAAAGGAGCTGCGGAGAACCCAGCATGATGAGAGCGCTTGGAGAGTGAAGAA 1800
QY 1738 CAGGTACAGTCAATGAATCAAGCTGAGCTGCTCACTAGACATCTATCAAG 1791
DB 1801 CAGGTCTTGTCCATGAGAAAGAGCTCGACTTCTTGTGATGATCTATCAAG 1854

RESULT 9
US-09-495-050A-303
Sequence 303, Application US/09495050A
Patent No. 6492505
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: US/09/495,050A
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 303
LENGTH: 582
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

Query Match 16.6%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 5,4e-143;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1630 GGAAGAGGCAATCATCATGATAAGAGCGAGAGAAATTAACAGCAGAACATGAG 1689
DB 1 GGAAGAGGCAATCATCATGATAAGAGCGAGAGAAATTAACAGCAGAACATGAG 60
QY 1690 ACCAGAGAGATCTCATGATGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1749
DB 61 ACCAGAGAGATCTCATGATGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 1750 ATGAGATCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1809
DB 121 ATGAGATCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 180
QY 1810 GCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1869
DB 181 GCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 1870 GACTATCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1929
DB 241 GACTATCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 1930 TTATCCAGATCACTAGTGCACATCTGAGAGGCTGCACTTCTGAGCCCAAT 1989
DB 301 TTATCCAGATCACTAGTGCACATCTGAGAGGCTGCACTTCTGAGCCCAAT 360
QY 1990 GAGTTGAGTCCAGACTTTCTAGCGGCTTACGCTTACGATGACAGTCAACACAG 2049
DB 361 GAGTTGAGTCCAGACTTTCTAGCGGCTTACGCTTACGATGACAGTCAACACAG 420
QY 2050 GAGCCAAATTAAGTCAAGGATGGCTGAGAGTGGGACCAACCAACCAACCAACCA 2109
DB 421 GAGCCAAATTAAGTCAAGGATGGCTGAGAGTGGGACCAACCAACCAACCAACCA 480
QY 2110 ATTAATACGCAACCAAGCAGAGCCCAACCAACTTTACAGATC 2154
DB 481 ATTAATACGCAACCAAGCAGAGCCCAACCAACTTTACAGATC 524

RESULT 10
US-09-105-058C-1
Sequence 1, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:

APPLICANT: Blonar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gridkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 896
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-09-105-058C-1

Query Match 15.2%; Score 465.4; DB 3; Length 896;
Best Local Similarity 53.7%; Pred. No. 1.9e-129;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;

QY 199 AGCCAGAGCTCCGCGCAAGTCAAGTACCGCGGCTGAGAACTTACTTCAACAGTG 258
DB 13 RGSMSCCMSYSAAGMMAAGCCMSYACCGMSMSYCARAMTTMTCTACACAGCS 72
QY 259 CTGAGAGACCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
DB 73 CTGAGAGACCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
QY 319 GATTCCTGATTTTGTCACTGTTTCTACATCCCTGAGCACACAAATTGGCCCTCAAGT 378
DB 133 KSTGCTGATTTTGTCACTGTTTCTACATCCCTGAGCACACAAATTGGCCCTCAAGT 191
QY 379 TGCTCTGATTCCTGAGTGTGATGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 438
DB 192 KSSCTTYSMTWTGGAAYMKYKRVATYKTSRVITVYGGHGBAGTWTYKYVTGMR 251
QY 439 ATCTGCTGCGGGTGTGCTGTTGCTGATATAGAGATGCAAGAACTGAGTTTCT 498
DB 252 ATCTGCTGCGGGTGTGCTGTTGCTGATATAGAGATGCAAGAACTGAGTTTCT 311
QY 499 CGAAGCCCTTCTGTATATAGATACATTTGTTTATCGCTTCAATAGAGTTTCT 558
DB 312 MGAARCCVCTSTGRTGATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 371
QY 559 GCAAAACTCAGGATTAATTTTGGCCAGCTGCTGCAAGTCTCCGTTTCTCAAG 618
DB 372 GYBGHMMWCARGGCAAGTGTGCAACVTCY---CTBCRAGCTGCTGCTGCTGCTGCTGCT 428
QY 619 ATCTCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
DB 429 ATYTRCGSATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
QY 679 GTTATGCTCAGAGCAAGATTAATCAAGCTTGTATCATAGATTTTGTGTTTAT 738
DB 489 RTCTRYGCTCAGAGCAAGATTAATCAAGCTTGTATCATAGATTTTGTGTTTAT 548
QY 739 TTTTGTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798
DB 549 CTKCYTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
QY 799 GGAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 858
DB 609 GCGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668

QY	855	UCCCTAACTTGGCTGGGAAGATTGTTTCTGACAGGCTTTGCACCTCTTGCAATTTCTTTC	918
Db	669	CCYAAFASTGGRAWGGSGMKCTSHTDGCVCAASTYWCCTYMATGGYGTCTCVTTY	728
QY	919	TTTGCACTTCCTGCGCGGCAATCTTGTCACAGTTTTCGATTAATAAGTACAAAGAACAC	978
Db	729	TTTGGCBCTKCCMGCDGSCATYTTGGGRCTCYGGSYTKGCCCTSAARGTCAAGAGACARAY	788
QY	979	CGCCAGAAACCTTTGAGAAAAAGAAAGAACCCAGCTGCACACTCATTCAGTGTGTTGG	1038
Db	789	MGKCARARCACTTTGAGAAHGGWGAABCCDGDGCMGBBCTSATYCAGKCKCCTGG	848
QY	1039	CCTAGTTACGACGACTGA	1055
Db	849	AGRTWYTAIVGCVACVAA	865

```

RESULT 11
US-09-177-650-90
? Sequence 90, Application US/09177650
? Patent No. 6413719
? GENERAL INFORMATION:
? APPLICANT: Leppert, Mark F.
? APPLICANT: Singh, Nanda
? APPLICANT: Charlier, Carole
? TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
? TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
? FILE REFERENCE: 2323-134
? CURRENT APPLICATION NUMBER: US/09/177,650
? CURRENT FILING DATE: 1998-10-23
? EARLIER APPLICATION NUMBER: 60/063,147
? EARLIER FILING DATE: 1997-10-24
? NUMBER OF SEQ ID NOS: 129
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 90
? LENGTH: 2814
? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (20) .. (2811)
? S-09-177-650-90

```

Query Match	15.1%	Score 463.6;	DB 3;	Length 2814;
Best Local Similarity	57.8%	Pred. No. 1.6e-128;		
Matches 951; Conservative	4;	Mismatches 623;	Indels 66;	Gaps 5;

QY	24	GTGGGCGCCGGGGCAGAGTGTCTGTGAATCTGGACACCGCCAGAGGGCCACGGCTCTGTACT	83
Db	294	GGCGGTGGCCCGCGCAGCAGAGACGGAAAGTGGGCTGTGCGCCAGGAGACGTGGAGCAAGT	353
QY	84	GCTGGGCAACCCGCGCGGCCACGCTTGTGTGGCGCGCGCGCGTGGACCTGAGGAGAGCGCGCG	143
Db	354	CACCTTGGCGCTTAGAGGGCGCCGAGCGCAACAAAGAACGAGACCTGCTGTCTGGAGGGCGGTGG	413
QY	144	GGGCAAGAGAGGGGGCGCGGATGAGCGCTGTGGGGGAAGCGCTCTCTTACAGAGTAGGCA	203
Db	414	CCGCGAAGAGGGGGCAGAGAGAGAACCCCGCAGGGCATCGGGCTTCTGGCGAAGAACCCCTCT	473
QY	204	GAGCTGCC-----GGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTACAA	254
Db	474	GAGCGCGCCCACTCAAGAGGAACAACGCCMAGTACAGGGCGCATCCMAACTTGTGATCTAAGA	533
QY	255	CGTGGTGAGAGACCCCGCGCTGGGCGCTTATCTACACGCTTTGTTTTCTCTGT	314
Db	534	CGCCCTGAGAGAACCGCGGGGCTGGGCGCTGCTCTACACGCGCTGTGTCTCGATTGT	593
QY	315	CTTTGTGTCTTGAATTTTGTCAGTGTTTCTTACCAATCCCTTAGACACACAAATATGGCCTC	374
Db	594	CTGGGAATGCTTGATTTCTGGCCGTGCTACCACTTCAAGGAATAATAGACTGTGTCTGG	653

OY	375	AAGTTGCTCTGTAATCTCGAGGTTCCGATGATTTGTGCTCTTTGGTTTGGAGTTTCATCAT	434
Db	654	AGACTGGCTTTTGTGTGCTGGAAACATTTGCTATTTTTCATCTTTTGAAGCTGAGTTTGTCTT	713
OY	435	TCGAATCTGGCTCGCGGGTTGCTGTTCGCTATATAGAGATGGGAAGGAAGACTGAGGTT	494
Db	714	GAGATCTGGGCTCGAGGATTTGCTGTCCATACAAAGGCTGGGCTGAGCGGCTAAAGTT	773
OY	495	TGCTCGAAAGCCCTTCTGTGTATATAGATACCATTTGTTCTTATCGCTTCAATAGCAGTTGT	554
Db	774	TGCCAGGAAGCCCTGTGCAATGTTGGAATCTTGTGTACTGATTTGCTCTGTGGCCAGTGT	833
OY	555	TTCTGCAAAACTAGAGGTATATTTTTCGCAAGCTGTGCACTAGAAAGTCTCGGTTTCTCT	614
Db	834	TGCGGTGGAAACCAAGGCAATGCTTGGCCACT---CCCTGGAAAGCCCTCGGCTTCT	890
OY	615	ACAGATCCTCCGCAATGGTGCGCATAGAACCGAAGGGAGAGCACTTGAATATTAATCGGGTTC	674
Db	891	GCAGATCTTGCGGCATGCTTGCATAGATAGAGAGGGGTGGCACTTGGAAAGCTCTGGGCTC	950
OY	675	AGTGATTTATGCTCACAGCAAGAAATTAATCAAGCTTGGTACATAGAGATTTTGTCTT	734
Db	951	GGCTATCTGTGCCACAGAAAGACTCATCAGCTCGGTGGATATAGGCTTCTGACACT	1010
OY	735	TATTTTTTCGTTCTTCTGTCTATCTGTGTGAAAGAGTG-----	775
Db	1011	CATCCCTTCTTCATTTCTTGTCTTGTCTACCTGTGTGAAGAGATGTGCAAGAAATGATGCCA	1070
OY	776	-----CCAATAAGAGTTTCTTCACTATGCAAGATGCTCTGTGTGGGACCAAT	824
Db	1071	AGGAGAGGATATGAAGGAGGATTTGAGCCTTATGCAATGCTTGTGTGTGGGCTGTGAT	1130
OY	825	TACATTGCAACTATTTGGCTATGAGACAAAACTCCCTTAATCTTGCTGGAGAGATTGCT	884
Db	1131	CACACTGGCCACCATTTGGTTATGAGACRAGACACTAAACCTGGGAAGGACTGTGAT	1190
OY	885	TTCTGCAGGCTTTCGACTCTCTTGGCAATTTCTTCTTTTGCACTTCTGCGGCATTTCTGG	944
Db	1191	TGCTGCCACCTTTTCTTTAATCGGCGCTCTCTTTTGTGCTTCCGCGAGGCAATCTTGG	1250
OY	945	CTCAGGTTTGCATTAATAAGTACAAAGAACACACCGGACAGAAACCTTGAAGAAAG	1004
Db	1251	CTCAGAGCTGCACTGAAGGTTGACGGAGCACACCTGACAGACATTTGAGAGAGAG	1310
OY	1005	GAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCTAGTTACGCACTGATGAGAATC	1064
Db	1311	GAACTGAGCTGCGGAATCTCATCCAGGCTGCTGAGAAATTTATCTACCAACCCCAAG	1370
OY	1065	TGTTTCCATTCGAACTTGGAAGCACACTTGAAAGCCTTGACACTGCGAGCCTTACCA	1124
Db	1371	GTTGGAATCTGGTGGCAACTGGAAGATCTTATGATCAAGTTGTCTTTCCTATCTTTCAG	1430
OY	1125	GAAAGAACAGGGGAACATCAACCACTCAGAGCTTAACTTAAAGAGGAGCGCCAT	1184
Db	1431	GAAAGAACATGTGAACACAGACGACCAAAACCTGGGCTCTTGTGATGGGTTTCCTT	1490
OY	1185	GGCTAGCCCCGAGGGCCAGAGTATTTAAGGCGCAAGACTCAGTAGTGACAGAGATGC	1244
Db	1491	TTCTTAATCTGTGTGATATCTAA-----AGGAAAGCTATTTAC	1532
OY	1245	CCCAAGACCGACATCAAGCCGAGGGCACTCCACCAAAAGTGAGAGCTGAGACTT	1304
Db	1533	CCCTCTGAATGTAGATGCCATAGAGAAAGCCCTTCCAAAGAGCCAAAGCCTGTGGCTT	1592
OY	1305	CAAGGACCGAAACCGGCTTCCGGCCCTGCTGGCGCTCAAAAGTTCTCAGCCAAACAGT	1364
Db	1593	AAACAAATTAAGAGGTTTCCGCAACCGCTTCTCGATTAAGCCTACGCTTTCTGGCAGAG	1652
OY	1365	GATGATGCTGACACAGCCCTTGGCACTGATGATGATATATGATGAAAAAGATGCCAGTG	1424
Db	1653	WTCGGAAGATGCTGGGACAGGCCACC-----CATGGCAGAAAGACAGGGGCTATGGGAA	1706
OY	1425	TGATGTATCAGTGGAAGCTCAACCCACCACTTAAACCTGTCAATTCAGCTATCAGAAT	1484

Db 1707 TGACWTCCTCATTTGMAAGACTGATCCCTCCCTWMAAGCGTCGATCCGAGCTGTGCAAT 1766
Qy 1485 TATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGAACTTACGTCATATGATGATAA 1544
Db 1767 TCTACAGTTCCTGCTATATATAAAAAAGTTCAAGAGAGAGCGTTAGAGCCCTTAATGATGTGA 1826
Qy 1545 AGATGTCATTGAAACAATATTTCTGTGTCATCTGACATGTTGTGTAGAAATTAAGAGCT 1604
Db 1827 AGATGTGATTTGAGCACTATTTCCGCGGACATCTTGACATGCTTTCCAGAGATTAAGTACCT 1886
Qy 1605 TCAACACGCTGTGATCAATTCT 1628
Db 1887 ACAGACAAGATGATATGATTTT 1910

RESULT 12
US-09-105-058C-26
Sequence 26, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blanner, Michael A.
APPLICANT: Dworeszky, Steven
APPLICANT: Griskoif, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Men-Pin
TITLE OF INVENTION: KClO4 POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 26
LENGTH: 2565
TYPE: DNA
ORGANISM: Homo sapiens
US-09-105-058C-26

Query Match 15.0%; Score 460.8; DB 3; Length 2565;
Best Local Similarity 57.9%; Pred. No. 1.1e-127;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

Qy 433 ATTGAATCTGTGCTGCGGGTTGCTGTGCTATAGAGATGGCAAGAACTGAGG 492
Db 463 TTGAGATCTGTGGCTGTGAGATGTTGTGCGATCAAAAGGTGGCGGGCCGACCTGAG 522
Qy 493 TTTGCTCGAAAGCCCTTCTGTATATAGATACCATTTGTTTATTCGCTTCAATAGCAGTT 552
Db 523 TTTGCGAAGAAAGCCCTGTGATGTGAGACATCTTTGTGTGATTTGCTGTGCGAGTG 582
Qy 553 GTTTTGTGCAAAACCTCAGGGTAAATTTTGGCAGCTGTGCACTCAGAAAGTCCGTTTC 612
Db 583 GTTGTGTGGGAAACCAAGGCAATGTTCTGGCACTT---CCCTGCAAGCCCTGGGCTTC 639
Qy 613 CTACAGATCTCCGCGATGTGGCATGAGACCGAAGGGAGGCACTTGAATATTTAGGAT 672
Db 640 CTGCAGATCTGCGCATCTGCGATGTGAGACCGGAGAGGTGGCACTTGAAGCTTTGGGC 699
Qy 673 TCAAGGTTTATGCTCAGAGCAAGGAATTAATCAGAGCTTGTATCATAGATTTTGTGTT 732
Db 700 TCAGCCATCTGTGCGCACAGCAAAAGACATCAGCGCTGGTACATCGGTTTCTGACA 759
Qy 733 CTATATTTTGTGCTTTCTGTTGTCTATCTGGTGAAGAAAGATGCC----- 777
Db 760 CTGATCTTTCTTCAATTTCTGTCTACCTGTGTGAAGAAAGCTCCAGAGGTGATGCA 819
Qy 778 -----AATPAAGATTTTCTACATATGAGATGCTCTGTGGGGCACA 822
Db 820 CAAGAGAGAGATGAAGAAAGAGTTTGAACCTTGTGAGATGCTGTGTGGGGCCCTG 879
Qy 823 ATTACATTGACAACATATTTGGCTATGAGACAAAATCCCTTAATCTTGGCTGGAAAGATTG 882
Db 880 ATCAGACTGGCCACCATTTGGCTATGAGACAAACCAACCAAGCGTGGAAAGGCCGTCTG 939
Qy 883 CTTCCTGAGGCTTTGCACTCTGGGCAATTTCTTTTGTGCACTTCCGCGGCAATCTT 942
Db 940 ATTGCGGCACTTTCTTAAATGTGGCTCTCTTTTGTGCTTCCAGCGGCAATCTG 999
Qy 943 GGCTCAGGTTTGTGCTTAAAGTACAAAGAACACCCGCGAAGAAACATTGTGAGAAAGA 1002
Db 1000 GGGTCCGGGCTGGCCCTCAAGGTGAGAGCAACCCCTCAAGAACCTTTGAGAAAGAG 1059
Qy 1003 AGGAACCCAGCTGCCAATCTTCAATTCAGTGTGTTGGCGTATGACGAGCTGATGAGAA 1062
Db 1060 AGGAAGCCAGCTGTGAGCTCATTCAGGCTGCTGAGAGTATTTATGATCAACACCCAAAC 1119
Qy 1063 TCTGTTTCATTTGCAACTGTGAAGCCACATTTGAAGGCTTGTGCAACCTGCAAGCCCTACC 1122
Db 1120 AGGATTTGACTGTGGCGCATGTGAGATTTTATGAAATGATGCTCTTTTCTTTCTTC 1179
Qy 1123 AAGAAAGAAAGAGGAGAGCATCAAGCAGTCAAGCTTAAGTTTAAAGAGAGAGTGGCGC 1182
Db 1180 AGGAAGAAAGAGCTGAGAGGAGCATCCAGCCAAAGAGCTGGGGCTTTGGATGGGGTTGGC 1239
Qy 1183 ATGCTAGCCCGAAGGGGCCAGATTTTAAGAGCCGACAGAGCTCAGTAGGTGACAGAGAG 1242
Db 1240 CTTTCTAATCTCGTGTGATGAGAAATACTAA-----AGGAAGCTAATTT 1281
Qy 1243 TCCCCAAGCAGCATCATCAGCGAGGCGAGTCCCAAGTAGTCAAGAGCTGAGAGC 1302
Db 1282 ACCCTCTGAATGTAGATGCCATGAAGAAAGTCTTTTAAAGAACAAAGCTGTGTGGC 1341
Qy 1303 TTCAACGACGAAACCCGCTTCGCGCCCTGCTGAGGCTCAAAAGTTCTCAGCAAAACCA 1362
Db 1342 TTAACAAATTAAGAGCGTTTCGACAGGCTCTTCGCAATGAAGAGCT-----AGCTTTTC 1395
Qy 1363 GTGATGATGCTGACACAGCCCTTGGCATGTATGATGATGATGATGATGATGATGATGATG 1422
Db 1396 TGGCAGATTTCTGAAGATGCGGGGACAGGTGACCCCATGGCGGAAGAGAGGGGCTATGGG 1455
Qy 1423 TGTGATGATCAGAGGAAGACCTCACCCACCACTTAAGCTGATTTGAGCTATTCAGA 1482
Db 1456 AATGACTTCCCATGGAAGACATGATCCCAACCTGAAGAGCGCGGACCTCGAGC 1515


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QY 1123 AAGAAAGCAAGGGGAGCATCAGACGTGAGAGCTTAAGTAAAGGAGCGAGTGGC 1182
DB 1252 AGGAAAGCAAGCTGAGGAGGAGCATCCAGCAAAAGCTGGTCTTGGATCGGGTCCG 1311
QY 1183 ATGGCTAGCCCGGAGGGGCGCAGAGTATTAAGAGCCGCAAGGCTCAGTAGGTGACAGAGG 1242
DB 1312 CTTTCTTAATCTCTGTGGTAGCACTA-----AGAAAGCTAATTT 1353
QY 1243 TCCCAAGACCGACATCAAGCCGAGGCGAGTCCGACAAAGTGCAGAAAGCTGGAGC 1302
DB 1354 ACCGCTCTGAATGTAGATGCGCATAGAAAGAAAGTCTTTTAAGAACAAAGCCTGTGGC 1413
QY 1303 TTGAAGACCGAAGCCGCTCCGCGCTCGCTCGCTCAAAAAGTTCTACGCAAAACA 1362
DB 1414 TTAAACAAATTAAGAGGCTTCCCGACGCGCTTCGATGAAGCCT-----ACGCTTTC 1467
QY 1363 GTGATGATGCTGACAGCCCTTGGCAGTGAATGATGATGAATAAAGAGTCCAG 1422
DB 1468 TGGCAGAGTCTTAAGATGCCGGAACAGGTGACCCATGGCGGAGACAGGGGCTATGGG 1527
QY 1423 TGTGATGATCAAGTGAAGACCTCACCCGACCACTTAAACTGTCAATTCGAGCTATCAGA 1482
DB 1528 AATGACTTCCCATCGAAGACATGATCCGACCTGAAGCGCGCATCCGAGCCGTGACA 1587
QY 1483 ATTATGAATTTTATGTTGCAAAACGAAAGTTTAAGAAACRTTACGTCATATGATGA 1542
DB 1588 ATTCTCAATTCGCTCTCTATTAATAAATAATCAAGAGACTTTGAGGCTTACGATGTG 1647
QY 1543 AAGATGTCATTAACAATATCTGCTGTCATCTGAGCATGTTGATGAATTAAGC 1602
DB 1648 AAGATGTGATTAAGAGATTTTCCCGGCGATCTGACATGCTTTCCAGATAAAGTAC 1707
QY 1603 CTTCAACAACGTTGTGATCAATTC 1628
DB 1708 CTTCAAGACGAATAGATATGATTTT 1733

RESULT 14
US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 305
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006f6
; LOCATION: 486, 510, 552, 573
; OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305
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Query Match 14.7%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 1,5e-125;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;
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QY 1630 GAAAAAGGCAATCATCATGATAGAGAGCGGAGAAATTAACAGCAGAACTGAG 1689
DB 1 GAAAAAGGCAATCATCATGATAGAGAGCGGAGAAATTAACAGCAGAACTGAG 60
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QY 1690 ACCACAGACATCTCAGATATGCTCGGTGGGTGTCAAGATTGAAAAAAGGTACATCC 1749
DB 61 ACCACAGACATCTCAGATATGCTCGGTGGGTGTCAAGATTGAAAAAAGGTACATCC 120
QY 1750 ATAGATCCAGCTGAGTGGCTTACTAGACATCTTAACAAGGCTCTCGAAAGGCTCT 1809
DB 121 ATAGATCCAGCTGAGTGGCTTACTAGACATCTTAACAAGGCTCTCGAAAGGCTCT 180
QY 1810 GCTCAGCCCTGCTTTGGCTTCAATTCAGTTCCGACCTTTTGAATGTGAACAGACATCT 1869
DB 181 GCTCAGCCCTGCTTTGGCTTCAATTCAGTTCCGACCTTTTGAATGTGAACAGACATCT 240
QY 1870 GACTATCAAGCCCTGTGTGATAGCAAAAGTCTTTGGGTTCCGCAAAAAGTGGCTGC 1929
DB 241 GACTATCAAGCCCTGTGTGATAGCAAAAGTCTTTGGGTTCCGCAAAAAGTGGCTGC 300
QY 1930 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCGAGTTGATTTCTGACGCAAT 1989
DB 301 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCGAGTTGATTTCTGACGCAAT 359
QY 1990 GAGTTCAGTGCACAGACTTCTACGCGCTTACGCTTACCTATGACAGTCAAGCAACAG 2049
DB 360 GAGTTCAGTGCACAGACTTCTACGCGCTTACGCTTACCTATGACAGTCAAGCAACAG 417
QY 2050 GTGCAATTAGTCAAGGAGTGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2109
DB 418 GTGCCAA-TAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 475
QY 2110 ATAAATAGGGACCCCAAGCCGACGAGCCCAACACTTAAAGATCCGACCTCTCT 2165
DB 476 ATAAATAGGGACCCCAAGCCGACGAGCCCAACACTTAAAGATCTCTCTGAGCTCT 531

RESULT 15
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaumer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19
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Query Match 13.8%; Score 425; DB 3; Length 3287;
Best Local Similarity 64.7%; Pred. No. 8.3e-117;
Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0;
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 Job time : 349.985 secs

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; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629

; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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US-10-661-629-1

Query Match 99.0%; Score 3040.4; DB 19; Length 3137;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3041; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      2701 CATTTTCTTCCAGGATAGCAGTTCCTTAGCCATATCATTCATTTGACATGAACTATTTCG 2760
QY      2770 AAAGCCCTTCTAATAAGTTGAAATTTGCAAGATGGGAGAAACATGAAGGCAAGTTTATA 2829
Db      2761 AAAGCCCTTCTAATAAGTTGAAATTTGCAAGATGGGAGAAACATGAAGGCAAGTTTATA 2820
QY      2830 AGCCCGTTACCTTTAATTTGATGAGAAATGCAATGTTTAAAGGATGGCTAAATTTCCAAAGT 2889
Db      2821 AGCCCGTTACCTTTAATTTGATGAGAAATGCAATGTTTAAAGGATGGCTAAATTTCCAAAGT 2880
QY      2890 GCATGACATTTAACCACTCATTTTAGTAATGTATACCTTGAAGTTAAAAAGCCTGAGAAACA 2949
Db      2881 GCATGACATTTAACCACTCATTTTAGTAATGTATACCTTGAAGTTAAAAAGCCTGAGAAACA 2940
QY      2950 AACACAGCTAATGCTATGGGGTGTATGAAATATGTCAAAGTTTAAAGTCAATTTGAAGATTG 3009
Db      2941 AACACAGCTAATGCTATGGGGTGTATGAAATATGTCAAAGTTTAAAGTCAATTTGAAGATTG 3000
QY      3010 ACACGTATTTTGAATTTATGGGAGTAAACACTTCAAAATTTCA 3053
Db      3001 ACACGTATTTTGAATTTATGGGAGTAAACACTTCAAAATTTCA 3044
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RESULT 3
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Query Match      94.1%; Score 2890.8; DB 9; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

QY      1 GGCAGCGGCATGAAGATGTGAGTGGGCGGCGGCGAGGGTGTCTGTAACCTGGCAGCC 60
DB      156 GGCAGCGGCATGAAGATGTGAGTGGGCGGCGGCGAGGGTGTCTGTAACCTGGCAGCC 215
QY      61 GCCAGGGGCGAGCGGCGTCTACTGCTGGGCAACCGGCGGCGCAACGCTGGTGGCGGCGGC 120
DB      216 GCCAGGGGCGAGCGGCGTCTACTGCTGGGCAACCGGCGGCGCAACGCTGGTGGCGGCGGC 275
QY      121 GGTGGCGCTGAGGAGAGCCCGCGGCGCAGAGGGGCGCGATGAGCCTGTCTGGGGAAG 180
DB      276 GGTGGCGCTGAGGAGAGCCCGCGGCGCAGAGGGGCGCGATGAGCCTGTCTGGGGAAG 335
QY      181 CGCCTCTCTTACACGAGTACCGAGCTGCCGCGCAACCTCAAGTACCGGCGGGTGCAG 240
DB      336 CGCCTCTCTTACACGAGTACCGAGCTGCCGCGCAACCTCAAGTACCGGCGGGTGCAG 395
QY      241 AACTACCTGTACAAGCGTGTGAGAGACCCCGGCGGCGTTCATCTTACACACGCTTTC 300
DB      396 AACTACCTGTACAAGCGTGTGAGAGACCCCGGCGGCGTTCATCTTACACACGCTTTC 455
QY      301 GTTTTCTCCTTCTTGGTGTCTGATTTTGTCAAGTGTTCATCCATCCTGTAGACAC 360
DB      456 GTTTTCTCCTTCTTGGTGTCTGATTTTGTCAAGTGTTCATCCATCCTGTAGACAC 515
QY      361 ACAAATTTGGCTTCAAGTTGCTCTTGATCTTGAAGTGTGTATGATTTGCTCTTGGT 420
DB      516 ACAAATTTGGCTTCAAGTTGCTCTTGATCTTGAAGTGTGTATGATTTGCTCTTGGT 575
QY      421 TTGAGGTCTATCATTTGGAATCTGCTGCGGGTGTGCTGTGTGATATGAGGATGGCAA 480
DB      576 TTGAGGTCTATCATTTGGAATCTGCTGCGGGTGTGCTGTGTGATATGAGGATGGCAA 635
QY      481 GGAAGA CTGAGGTTGTCTGCAAGCCCTTCTGTATTATAGATCAATGTTCTTATCGCT 540
DB      636 GGAAGA CTGAGGTTGTCTGCAAGCCCTTCTGTATTATAGATCAATGTTCTTATCGCT 695
QY      541 TCAATTGCAATGTGTTCTGCAAAAACCTCAGGGTAATATTTTGGCAGCTGTGACATCAGA 600
DB      696 TCAATTGCAATGTGTTCTGCAAAAACCTCAGGGTAATATTTTGGCAGCTGTGACATCAGA 755
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QY      601 AGTCTCGGTTTCTCTACAGATCCCTCGCATGTGGCGCATGGACCGAAGGGGAGCACTGG 660
DB      756 AGTCTCGGTTTCTCTACAGATCCCTCGCATGTGGCGCATGGACCGAAGGGGAGCACTGG 815
QY      661 AAATTACCTGGGTTCACTGGTTTATGCTCAACAGCAAGAAATTATCAACAGCTTGTATATA 720
DB      816 AAATTACCTGGGTTCACTGGTTTATGCTCAACAGCAAGAAATTATCAACAGCTTGTATATA 875
QY      721 GGAATTTTGGTCTTATTTTGTGCTCTTCTCTTCTTCTATCTGTGTGAAAAAGATGCCAAT 780
DB      876 GGAATTTTGGTCTTATTTTGTGCTCTTCTCTTCTTCTATCTGTGTGAAAAAGATGCCAAT 935
QY      781 AAAGATTTTCTACATATGACAAGTGTCTCTGTGTGGGACAAATTATCATTTGACAACTATT 840
DB      936 AAAGATTTTCTACATATGACAAGTGTCTCTGTGTGGGACAAATTATCATTTGACAACTATT 995
QY      841 GGCTATGAGACAAAACCTCCCTTACTGTGCTGGGAAGATGCTTTCTCAGGCTTTTGA 900
DB      996 GGCTATGAGACAAAACCTCCCTTACTGTGCTGGGAAGATGCTTTCTCAGGCTTTTGA 1055
QY      901 CTCTTGGCATTTCTTCTTTTGTGACTTCTGCGGCAATCTTGCTCAGGTTTGCATTA 960
DB      1056 CTCTTGGCATTTCTTCTTTTGTGACTTCTGCGGCAATCTTGCTCAGGTTTGCATTA 1115
QY      961 AAAGTACAAGAACCAACCGCGGAGAAACATTTGAGAAAAGAAAGAACCCAGCTGCCAAC 1020
DB      1116 AAAGTACAAGAACCAACCGCGGAGAAACATTTGAGAAAAGAAAGAACCCAGCTGCCAAC 1175
QY      1021 CTCAATTCACTGTGTTTGGCGTATTAACGAGCTGATGAGAAATCTGTTCATTGCAATC 1080
DB      1176 CTCAATTCACTGTGTTTGGCGTATTAACGAGCTGATGAGAAATCTGTTCATTGCAATC 1235
QY      1081 TGAAGCCCACTTTGAAGGCTTTGCACACCTGACGCTTCAACCAAGAAACAAGGGGAA 1140
DB      1236 TGAAGCCCACTTTGAAGGCTTTGCACACCTGACGCTTCAACCAAGAAACAAGGGGAA 1279
QY      1141 GCATCAAGCAGTCAGAAAGTTAAGTTTAAAGACGAGTGCAGATGGCTAGCCCAAGGGC 1200
DB      1280 -----TCAGAGCTTAAGTTTAAAGACGAGTGCAGATGGCTAGCCCAAGGGC 1328
QY      1201 CAGAGTATTAAAGCCGACCAAGCTTCAGTAGGTGACAGAGGTGCCCAAGCAACCAATC 1260
DB      1329 CAGAGTATTAAAGCCGACCAAGCTTCAGTAGGTGACAGAGGTGCCCAAGCAACCAATC 1388
QY      1261 ACAGCCGAGGAGAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACCAAGCAACCCGC 1320
DB      1389 ACAGCCGAGGAGAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACCAAGCAACCCGC 1448
QY      1321 TTCGGGCGCTGCTGCGGCTCAAAAAGTTCTCAGCCCAAAACCAAGTGA TAGATGTCAGACA 1380
DB      1449 TTCGGGCGCTGCTGCGGCTCAAAAAGTTCTCAGCCCAAAACCAAGTGA TAGATGTCAGACA 1508
QY      1381 GCCCTTGGCAGTATGATATATGATGAAAAAGATGCGAGTGTATCAATGAGAA 1440
DB      1509 GCCCTTGGCAGTATGATATATGATGAAAAAGATGCGAGTGTATCAATGAGAA 1568
QY      1441 GACCTCAACCCCAACCTTAAACCTGTCAATTGCAAGCTTATAGAAATTTCAATGTT 1500
DB      1569 GACCTCAACCCCAACCTTAAACCTGTCAATTGCAAGCTTATAGAAATTTCAATGTT 1628
QY      1501 GCAAAAACGGAAGTTTAAAGAAACRTTACGTCAATATGATGTAAGAAAGATGTCATTGAACA 1560
DB      1629 GCAAAAACGGAAGTTTAAAGAAACRTTACGTCAATATGATGTAAGAAAGATGTCATTGAACA 1688
QY      1561 TATTCTGTGATCATCTGAGCATGTTGTGTAGAAATTAAGCCCTTCAACACGTTGTAT 1620
DB      1689 TATTCTGTGATCATCTGAGCATGTTGTGTAGAAATTAAGCCCTTCAACACGTTGTAT 1748
QY      1621 CAAATTTCTGGAAGAGGCAATTCATCAATGATTAAGAAAGCCGAGAGAAATAACAGCA 1680
DB      1749 CAAATTTCTTGAAGAGGCAATTCATCAATGATTAAGAAAGCCGAGAGAAATAACAGCA 1808
QY      1681 GAACATGAGACACAGACGATCTCAGTATGCTCGGTGCGGTGTGCAAGTTGAAAAACAG 1740
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Db	1809	GAACATGAGACCAACGACGATCTCGATATGCTCGGTCCGGTGGTCCAGGTTGAAAAACAG	1868
Qy	1741	GTACAGTCCATAGAAATCCAAAGCTGACTGCTTAAATCTATCAACAGATCTCTCGG	1800
Db	1869	GTACAGTCCATAGAAATCCAAAGCTGACTGCTTAAATCTATCAACAGATCTCTCGG	1928
Qy	1801	AAAGGCTCTGGCTCAGCCCTCGCTTTGGCTTCAATTCAGATTGCCACTTTGGATTGTGA	1860
Db	1929	AAAGGCTCTGGCTCAGCCCTCGCTTTGGCTTCAATTCAGATTGCCACTTTGGATTGTGA	1988
Qy	1861	CAGACATCTGAATCTAAAGCCCTGTGTGATAGCAAAAGATCTTTGGGTTCCGCAAAAC	1920
Db	1989	CAGACATCTGAATCTAAAGCCCTGTGTGATAGCAAAAGATCTTTGGGTTCCGCAAAAC	2048
Qy	1921	AGTGGCTGCTTATCCAGATTCAACTAGTGTCCAAACATCTGGAAGGCTGTGCAATCTGTG	1980
Db	2049	AGTGGCTGCTTATCCAGATTCAACTAGTGTCCAAACATCTGGAAGGCTGTGCAATCTGTG	2108
Qy	1981	ACGCCAAATGAGTTCAGTGCCAGACTTTCTACGGCTTTAGCCCTCAATGACAGTCAAA	2040
Db	2109	ACGCCAAATGAGTTCAGTGCCAGACTTTCTACGGCTTTAGCCCTCAATGACAGTCAAA	2168
Qy	2041	GCAACACAGGTGTCCAAATTAATGTCMAAGCATAATGCTCAGCATGTGGCAGCCCAACCAAT	2100
Db	2169	GCAACACAGGTGTCCAAATTAATGTCMAAGCATAATGCTCAGCATGTGGCAGCCCAACCAAT	2228
Qy	2101	GCAAAACCAATTAATACGGCACCCAGCGACAGGCCCAACAACTTTACAGATCCCACT	2160
Db	2229	GCAAAACCAATTAATACGGCACCCAGCGACAGGCCCAACAACTTTACAGATCCCACT	2288
Qy	2161	CCTCTCCCAAGCATCAGCATCTGTGCCAGGCCAGAACTCTGCACCTTAACCTGTGACGC	2220
Db	2289	CCTCTCCCAAGCATCAGCATCTGTGCCAGGCCAGAACTCTGCACCTTAACCTGTGACGC	2348
Qy	2221	TTACAGGAAACATTTCTGACGTCAACCACTGCTGTGTGCTCCAAAGGAAATGTTTCAAG	2280
Db	2349	TTACAGGAAACATTTCTGACGTCAACCACTGCTGTGTGCTCCAAAGGAAATGTTTCAAG	2408
Qy	2281	GTTGCACAGTCAAAATCTCCACCAAGACCGTTCTATAGAGAAACCTTTGACATGTGAGGA	2340
Db	2409	GTTGCACAGTCAAAATCTCCACCAAGACCGTTCTATAGAGAAACCTTTGACATGTGAGGA	2468
Qy	2341	GAAATCTGTGTGTCTGTCTGTCCATAGTGTGCCAGAAACCTTTGGCAAACTTTTGTCTGTG	2400
Db	2469	GAAATCTGTGTGTCTGTCTGTCCATAGTGTGCCAGAAACCTTTGGCAAACTTTTGTCTGTG	2528
Qy	2401	CAAAACCTGATCAGGTCCGACCGAGAACTGAATATCAACTTTAGGGAGTGAATCAAGT	2460
Db	2529	CAAAACCTGATCAGGTCCGACCGAGAACTGAATATCAACTTTAGGGAGTGAATCAAGT	2588
Qy	2461	GGCTTCAGAGGACGCCAAGATTTTTATCCCAATGAGAGGAAATCCAAATGTTTATTAAT	2520
Db	2589	GGCTTCAGAGGACGCCAAGATTTTTATCCCAATGAGAGGAAATCCAAATGTTTATTAAT	2648
Qy	2521	GATGAAGAGGTGGGTGCCGAAAGAGACAGACACACTTTTGATGTGCCAGCGCAACT	2580
Db	2649	GATGAAGAGGTGGGTGCCGAAAGAGACAGACACACTTTTGATGTGCCAGCGCAACT	2708
Qy	2581	GCCAGGGAAGCTGCTTTGATCAGACTCTCTAAGACTGTGAAGACTGTGAAGTCAAGATCACTTCAG	2640
Db	2709	GCCAGGGAAGCTGCTTTGATCAGACTCTCTAAGACTGTGAAGACTGTGAAGTCAAGATCACTTCAG	2768
Qy	2641	AGCAATTTGTAAGAGAGAGAAAGTAACAGATGCCCTCAGCTTCATATCTAAATCTGA	2700
Db	2769	AGCAATTTGTAAGAGAGAGAAAGTAACAGATGCCCTCAGCTTCATATCTAAATCTGA	2828
Qy	2701	TAAATCTTCAATTTCTTTCCAGGCATAGCAATCTTTAGCCATACATATCATTTGATGATGA	2760
Db	2829	TAAATCTTCAATTTCTTTCCAGGCATAGCAATCTTTAGCCATACATATCATTTGATGATGA	2888
Qy	2761	ACTATTTTCGAAGCCCTTTTAAAAAGTTGAATTTGCAAGATCGGGAAGAAATGAAAGG	2820

Db	2889	ACTATTTCGAAAGCCCTTCTPAAAAGTTGAATTCGAAGAATCGGGAAGAACNTGAAGC	2941
OY	2821	CAGTTTATAAGCCCCGTGTAACCTTTTAAATTGCATGAAAAATGCATGTTTAGGGATGCGTAA	2880
Db	2949	CAGTTTATAAGCCCGTGTAACCTTTTAAATTGCATGAAAAATGCATGTTTAGGGATGCGTAA	3008
OY	2881	TTCCAAGTGATGCATTAACCACATTTAGTATGATACCTTGAGTTAAAAAGCT	2940
Db	3009	TTCCAAGTGATGCATTAACCACATTTAGTATGATACCTTGAGTTAAAAAGCT	3067
OY	2941	GAGAAACCAACACACAGC-TAATGCTATGGGTATGAAATATGT	2983
Db	3068	GAGAAACCAACACACAGCTTAATGCTATGGGGGTATGAATATGT	3111
 RESULT 4 US-10-803-268--3 ; Sequence 3, Application US/10803268 ; Publication No. US20040157259A1 ; GENERAL INFORMATION: ; APPLICANT: Hu, Yi ; APPLICANT: Kieke, James Alvin ; APPLICANT: Turner, C. Alexander Jr. ; APPLICANT: Nehls, Michael C. ; APPLICANT: Friedrich, Glenn ; APPLICANT: Zambrowsicz, Brian ; APPLICANT: Sands, Arthur T. ; TITLE OF INVENTION: Novel Human Ion Channel Protein and ; FILE REFERENCE: LEX-0160-USA ; CURRENT APPLICATION NUMBER: US/10/803,268 ; PRIOR FILING DATE: 2004-03-18 ; PRIOR APPLICATION NUMBER: US/09/825,147 ; PRIOR FILING DATE: 2001-04-03 ; PRIOR APPLICATION NUMBER: US 60/194,255 ; PRIOR FILING DATE: 2000-04-03 ; NUMBER OF SEQ ID NOS: 3 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 3 ; LENGTH: 3111 ; TYPE: DNA ; ORGANISM: homo sapiens US-10-803-268--3			
OY	1	GGCAGCGGCATGAAAGATGTGSAAGTCGGGCGCGGGCGAGGATGCTGTGAATCGGCAGCC	60
Db	156	GGCAGCGGCATGAAAGATGTGSAAGTCGGGCGCGGGCGAGGATGCTGTGAATCGGCAGCC	215
OY	61	GCCAGGGGCGACGGCGCTGTACTGTGGGACCCGCGCGCACGCTTGTGTGGCGCGC	120
Db	216	GCCAGGGGCGACGGCGCTGTACTGTGGGACCCGCGCGCACGCTTGTGTGGCGCGC	275
OY	121	GGTGGCTTGAGGGAGAGACGCCCGGGGCGAACAGAGGGGGCCCGGATGAAGCTCTGGGAA	180
Db	276	GGTGGCTTGAGGGAGAGACGCCCGGGGCGAACAGAGGGGGCCCGGATGAAGCTCTGGGAA	335
OY	181	CCGCTCTCTTAACAAGATGACCAAGATGCGCGGCGCAAAGTCAAGTACCGCGGGGTGAG	240
Db	336	CCGCTCTCTTAACAAGATGACCAAGATGCGCGGCGCAAAGTCAAGTACCGCGGGGTGAG	395
OY	241	AACACTCTGTACAACGTGCTGAGAGACCCCGCGGCTGGGCGTTTCATCTACACGCTTTC	300
Db	396	AACACTCTGTACAACGTGCTGAGAGACCCCGCGGCTGGGCGTTTCATCTACACGCTTTC	455
OY	301	GTTTTCTCCTTGCTTTGGTGTGATTTTGTACAGTGTTTTCTACATCCCGAGAC	360
Db	456	GTTTTCTCCTTGCTTTGGTGTGATTTTGTACAGTGTTTTCTACATCCCGAGAC	515
OY	361	ACAAATTTGGCCTCAAGTTGCCCTCTTGATCTCGAGATTCTGTATGATTTGCTTTGGT	420

|||||
Db 516 ACAAAATGGCTCAGATGCTCTGATCCTGGAGTTCGATGATGATGCTGCTTGGT 575
Qy 421 TTGGAGTTCATTCGAAATCGGTCTGGGGTGGCTGGTGGATTTAGAGATGGCAA 480
Db 576 TTGGAGTTCATTCGAAATCGGTCTGGGGTGGCTGGTGGATTTAGAGATGGCAA 635
Qy 481 GGAAGACTGAGTTCGTAAGAGCCCTCTGTGTATAGATACATGTTCTTATGCT 540
Db 636 GGAAGACTGAGTTCGTAAGAGCCCTCTGTGTATAGATACATGTTCTTATGCT 695
Qy 541 TCAATACAGTTCGTAAGAGCCCTCTGTGTATAGATACATGTTCTTATGCT 600
Db 696 TCAATACAGTTCGTAAGAGCCCTCTGTGTATAGATACATGTTCTTATGCT 755
Qy 601 AGCTCCGTTTCCAGAGATCCTCCGATGGTGGCATGGAACGGAAGGAGACCTGG 660
Db 756 AGCTCCGTTTCCAGAGATCCTCCGATGGTGGCATGGAACGGAAGGAGACCTGG 815
Qy 661 AAATTAAGTTCAGTTCGTAAGAGCCCTCTGTGTATAGATACATGTTCTTATG 720
Db 816 AAATTAAGTTCAGTTCGTAAGAGCCCTCTGTGTATAGATACATGTTCTTATG 875
Qy 721 GAATTTTGGTTCATTTTGTCTTCTGCTTCTGTCTATCTGTGAAAAGATGCCAT 780
Db 876 GAATTTTGGTTCATTTTGTCTTCTGCTTCTGTCTATCTGTGAAAAGATGCCAT 935
Qy 781 AAAGAGTTTCTATCATATGAGAGATCTCTGTGGGGGACAAATTAATGACAACTAT 840
Db 936 AAAGAGTTTCTATCATATGAGAGATCTCTGTGGGGGACAAATTAATGACAACTAT 995
Qy 841 GGCATATGAGACAAAATCCCTTAATCTGTGGTGGAGATGCTTCTGAGAGCTTGA 900
Db 996 GGCATATGAGACAAAATCCCTTAATCTGTGGTGGAGATGCTTCTGAGAGCTTGA 1055
Qy 901 CTCCTTGGCAATTTCTTTCTTTGCACTTCTGCGGCAATTTCTGCTCAGGTTTGA 960
Db 1056 CTCCTTGGCAATTTCTTTCTTTGCACTTCTGCGGCAATTTCTGCTCAGGTTTGA 1115
Qy 961 AAAGTACAAAGAACACCCGCCAGAAACATTTGAGAAAAGAAAGAAACCCAGCTGCCAAC 1020
Db 1116 AAAGTACAAAGAACACCCGCCAGAAACATTTGAGAAAAGAAAGAAACCCAGCTGCCAAC 1175
Qy 1021 CTCATTCAGTGTGTGGCGATGTAAGAGATGTAAGAAATCTGTTTTCATTTGCAACC 1080
Db 1176 CTCATTCAGTGTGTGGCGATGTAAGAGATGTAAGAAATCTGTTTTCATTTGCAACC 1235
Qy 1081 TGGAGCCACACTTGAAGGCTTGCACACTGCAAGCCCTTACAAAGAAAGAAAGAGGGA 1140
Db 1236 TGGAGCCACACTTGAAGGCTTGCACACTGCAAGCCCTTACAAAGAAAGAAAGAGGGA 1279
Qy 1141 GCATCAAGCAGTGAAGGCTTGAAGAGGAGTGGCATGGCTAGCCCGAGGGGC 1200
Db 1280 -----TCGAAGCTTAAGTTTGAAGAGGAGTGGCATGGCTAGCCCGAGGGGC 1328
Qy 1201 CAGAGTATTAAGGCGGCAAGGCTCAGTAGTGAAGAGAGTCCCAAGCAACGACATC 1260
Db 1329 CAGAGTATTAAGGCGGCAAGGCTCAGTAGTGAAGAGAGTCCCAAGCAACGACATC 1388
Qy 1261 ACAGCCGAGGAGTCCCAAGAGTGAAGAGGCTGAGCTTCAACGACGAAACCCGC 1320
Db 1389 ACAGCCGAGGAGTCCCAAGAGTGAAGAGGCTGAGCTTCAACGACGAAACCCGC 1448
Qy 1321 TTCCCGGCTCTGCTGGCTCAAAAGTTCTCAGCAAAACCAAGTATGATGCTGACACA 1380
Db 1449 TTCCCGGCTCTGCTGGCTCAAAAGTTCTCAGCAAAACCAAGTATGATGCTGACACA 1508
Qy 1381 GCCCTTGACACTGATGATATATGATGATAAAAGATGCCAGTGTATGATCAGTGA 1440
Db 1509 GCCCTTGACACTGATGATATATGATGATAAAAGATGCCAGTGTATGATCAGTGA 1568
Qy 1441 GACCTCACCCACCACTTAAACTGTCAATTCAGACTATCAGAAATTAAGAAATTCATGTT 1500

Db 1569 GACCTCACCCACCACTTAAACTGTCAATTCAGACTATCAGAAATTAAGAAATTCATGTT 1628
Qy 1501 GCAAAACGGAAGTTTAAGGAAACRTTACGTCATATGATGTAAGATGATGTAACAA 1560
Db 1629 GCAAAACGGAAGTTTAAGGAAACRTTACGTCATATGATGTAAGATGATGTAACAA 1688
Qy 1561 TATTCGTGCTGATCTGACATGTTGTGTAATTAAGCCCTTCAACACGCTGTGAT 1620
Db 1689 TATTCGTGCTGATCTGACATGTTGTGTAATTAAGCCCTTCAACACGCTGTGAT 1748
Qy 1621 CAATTCCTTGAAAAGGCGCAATACATCATGATTAAGAGCCGAGAGAAATTAACGCA 1680
Db 1749 CAATTCCTTGAAAAGGCGCAATACATCATGATTAAGAGCCGAGAGAAATTAACGCA 1808
Qy 1681 GAACATGAGCCACAGACATCTCAGTATGCTCGGTGGTCAAGGTGTAAGAAACAG 1740
Db 1809 GAACATGAGCCACAGACATCTCAGTATGCTCGGTGGTCAAGGTGTAAGAAACAG 1868
Qy 1741 GTACAGTCCATAGAAATCCAAAGCTGGAATGCTCTATGACATCTATCAACAGTCTTCGG 1800
Db 1869 GTACAGTCCATAGAAATCCAAAGCTGGAATGCTCTATGACATCTATCAACAGTCTTCGG 1928
Qy 1801 AAAGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGTTCACCTTTGAATGTA 1860
Db 1929 AAAGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGTTCACCTTTGAATGTA 1988
Qy 1861 CACACATCTGACATTAAGCCCTGAGATGAGAAAGATCTTCCGGTCCGACAAAC 1920
Db 1989 CACACATCTGACATTAAGCCCTGAGATGAGAAAGATCTTCCGGTCCGACAAAC 2048
Qy 1921 AGTGGCTGTTATCCAGATCACTAGTGCACATCTCAGAGGCTGAGATCATTTG 1980
Db 2049 AGTGGCTGTTATCCAGATCACTAGTGCACATCTCAGAGGCTGAGATCATTTG 2108
Qy 1981 AGCCCAATGAGTTCAGTGGCCAGACTTCTTACGCGCTTACCCCTATGACAGTCAA 2040
Db 2109 AGCCCAATGAGTTCAGTGGCCAGACTTCTTACGCGCTTACCCCTATGACAGTCAA 2168
Qy 2041 GCAACACAGTGCATTAAGTCAAGAGAGTGTGACAGTGGCAGCCACCAACACAT 2100
Db 2169 GCAACACAGTGCATTAAGTCAAGAGAGTGTGACAGTGGCAGCCACCAACACAT 2228
Qy 2101 GCAACCAATTAATTAAGGCAACCCAGAGCCAGCCCAACCACTTACAGATCCCACT 2160
Db 2229 GCAACCAATTAATTAAGGCAACCCAGAGCCAGCCCAACCACTTACAGATCCCACT 2288
Qy 2161 CCTCTCCAGCCATCAAGCATCTGCCAGGCAAGAACTTGTGACCTTACCTGAGGC 2220
Db 2289 CCTCTCCAGCCATCAAGCATCTGCCAGGCAAGAACTTGTGACCTTACCTGAGGC 2348
Qy 2221 TTAAGAGAAAGCATTTCTGACGTCACACCTGCTTGTGCTCCAAAGAAATGTTGAG 2280
Db 2349 TTAAGAGAAAGCATTTCTGACGTCACACCTGCTTGTGCTCCAAAGAAATGTTGAG 2408
Qy 2281 GTTGCACTGCAATCTCAGCAAGGACCGTTCTATGAGAAAGCTTTGACATGGAGGA 2340
Db 2409 GTTGCACTGCAATCTCAGCAAGGACCGTTCTATGAGAAAGCTTTGACATGGAGGA 2468
Qy 2341 GAAACTCTGTGTCTGTCTGTCCATGATGTCGGAAGAACTTGGCAAAATCTTGTCTGTG 2400
Db 2469 GAAACTCTGTGTCTGTCTGTCCATGATGTCGGAAGAACTTGGCAAAATCTTGTCTGTG 2528
Qy 2401 CAAAACCTGATCAGGTCGACGAGAACTGAAATATCACTTTCAAGAGTGTGATCAAGT 2460
Db 2529 CAAAACCTGATCAGGTCGACGAGAACTGAAATATCACTTTCAAGAGTGTGATCAAGT 2588
Qy 2461 GGCTCAGAGGACGCAAGATTTTACCCCAATGAGGAAATCCAAATTTGTTTAACT 2520
Db 2589 GGCTCAGAGGACGCAAGATTTTACCCCAATGAGGAAATCCAAATTTGTTTAACT 2648
Qy 2521 GATGAAGAGTGGTCCGAAAGACAGAGACACATTTTGTATGTCGACCGCAGCCT 2580
Db 2649 GATGAAGAGTGGTCCGAAAGACAGAGACACATTTTGTATGTCGACCGCAGCCT 2708

QY 2581 GCCAGGAAAGCTGCTTTGGCATCAGACTCTTAAGAGCTGGAAGGTCAAGATCATCTCAG 2640
DB 2709 GCCAGGAAAGCTGCTTTGGCATCAGACTCTTAAGAGCTGGAAGGTCAAGATCATCTCAG 2768
QY 2641 AGCATTTGTAAAGGAGAGAAAGTACAGATGCCCTCAGCTTGCATGTCAAACTGAAA 2700
DB 2769 AGCATTTGTAAAGGAGAGAAAGTACAGATGCCCTCAGCTTGCATGTCAAACTGAAA 2828
QY 2701 TAAGTCTTCATTTCTTTCCAGGCAATGAGTCTTTAGCCATACATATCATTTGATGA 2760
DB 2829 TAAGTCTTCATTTCTTTCCAGGCAATGAGTCTTTAGCCATACATATCATTTGATGA 2888
QY 2761 ACTATTTGAAAGCCCTTCTAAAGTGAATGTGAGAAATGGGAGAGAACTGAAAG 2820
DB 2889 ACTATTTGAAAGCCCTTCTAAAGTGAATGTGAGAAATGGGAGAGAACTGAAAG 2948
QY 2821 CAGTTATTAAGCCCTTACCTTTTAATGTGATGAAATGATTTAGGATGGCTAAA 2880
DB 2949 CAGTTATTAAGCCCTTACCTTTTAATGTGATGAAATGATTTAGGATGGCTAAA 3008
QY 2881 TTCAGAGTGCATGACATTTAACCTGATTAATGATGATGATGATGATGATGATGAT 2940
DB 3009 TTCAGAGTGCATGACATTTAACCTGATTAATGATGATGATGATGATGATGATGAT 3067
QY 2941 GAGAAACCAACACAGC-TAATGCTATGGGTGTATGAATATGT 2983
DB 3068 GAGAAACCAACACAGC-TAATGCTATGGGTGTATGAATATGT 3111

RESULT 5
US-09-813-148-1
Sequence 1, Application US/09813148
Patent No. US20020076809A1
GENERAL INFORMATION:
APPLICANT: STEINMEYER, Klaus
APPLICANT: LERCHE, Christian
APPLICANT: SCHERER, Constanze
APPLICANT: SEEBOM, Guiscard
APPLICANT: BUSCH, Andreas E.
TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF THE
TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
FILE REFERENCE: 38005-119
CURRENT APPLICATION NUMBER: US/09/813,148
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 100 13 732.6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/194,041
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-09-813-148-1

Query Match 93.0%; Score 2857.4; DB 9; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGCAGCGGATGATGAGATGTGAGTGGGCGGGGAGGAGTGTGCTGAATCTCGACAGCC 60
DB 206 GGCAGCGGATGATGAGATGTGAGTGGGCGGGGAGGAGTGTGCTGAATCTCGACAGCC 265
QY 61 GCCAGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 266 GCCAGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325
QY 121 GGTGGCTGAGGAGAGCGCGCGGGGCAAGAGGGGGCCCGGATGAGCTGCTGCGGGAAG 180
DB 326 GGTGGCTGAGGAGAGCGCGCGGGGCAAGAGGGGGCCCGGATGAGCTGCTGCGGGAAGC 385

QY 181 CCGCTCTCTTACACGAGTACGCCAGAGCTGCCGCGCAAGCTCAAGTACCGGGGCTGAC 240
DB 386 GCGCTCTCTTACACGAGTACGCCAGAGCTGCCGCGCAAGCTCAAGTACCGGGGCTGAC 445
QY 241 AACTACCTGTACAAAGTGTGAGAGACCCCGGCTGGGCTTCAATCAACGCTTTC 300
DB 446 AACTACCTGTACAAAGTGTGAGAGACCCCGGCTGGGCTTCAATCAACGCTTTC 505
QY 301 GTTTTTCCTCTGTCTTTGGTGTGCTGATTTTGTCAAGTATTTTCAACATCCCTGAGAC 360
DB 506 GTTTTTCCTCTGTCTTTGGTGTGCTGATTTTGTCAAGTATTTTCAACATCCCTGAGAC 565
QY 361 ACAAAATGGCTCAAGTTGCTCTTGAATCTGAGATTTGATGATGATGATGATGATGAT 420
DB 566 ACAAAATGGCTCAAGTTGCTCTTGAATCTGAGATTTGATGATGATGATGATGATGAT 625
QY 421 TTGAGTTCATCATTCGAAATCTGCTGTCGCGGTTTCTGTGCTATATAGAGATGGCA 480
DB 626 TTGAGTTCATCATTCGAAATCTGCTGTCGCGGTTTCTGTGCTATATAGAGATGGCA 685
QY 481 GGAAGACTGAGGTTGCTGAAAGCCCTTCTGTATATAGATACCATTTGCTATGCT 540
DB 686 GGAAGACTGAGGTTGCTGAAAGCCCTTCTGTATATAGATACCATTTGCTATGCT 745
QY 541 TCAATAGCAGTTTCTGCAAAAACCTGAGGTAATTTTTCAGCTTTCAGCTCAG 600
DB 746 TCAATAGCAGTTTCTGCAAAAACCTGAGGTAATTTTTCAGCTTTCAGCTCAG 805
QY 601 AGTCTCCGTTTCTCAAAATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 806 AGTCTCCGTTTCTCAAAATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 865
QY 661 AAATTAAGTGGTTCAGTGTATATGCTCAACAGCAAGATTAATCAAGCTTGTACATA 720
DB 866 AAATTAAGTGGTTCAGTGTATATGCTCAACAGCAAGATTAATCAAGCTTGTACATA 925
QY 721 GGAATTTTGGTTCATATTTTTCGTTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 780
DB 926 GGAATTTTGGTTCATATTTTTCGTTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 985
QY 781 AAAGGTTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 986 AAAGGTTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045
QY 841 GGCATGAGACAAACCTCCCTAATCTGCTGAGAAATGCTTTCGACAGCTTTCGA 900
DB 1046 GGCATGAGACAAACCTCCCTAATCTGCTGAGAAATGCTTTCGACAGCTTTCGA 1105
QY 901 CTCTTGGCAATTTCTTCTTTCGACTTCTGCGGCAATTTCTTGGCTCAAGTTTTCATTA 960
DB 1106 CTCTTGGCAATTTCTTCTTTCGACTTCTGCGGCAATTTCTTGGCTCAAGTTTTCATTA 1165
QY 961 AAAGTACAAAGAACACCGGCAAGAACATTTGAGAAAGAGAACCCAGCTGCAAC 1020
DB 1166 AAAGTACAAAGAACACCGGCAAGAACATTTGAGAAAGAGAACCCAGCTGCAAC 1225
QY 1021 CTCAATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1226 CTCAATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1285
QY 1081 TGAAGCCACCTTGAAGCCCTTGCACCTGACAGCCCTTACCAAGAAAGAACAGGGGAA 1140
DB 1286 TGAAGCCACCTTGAAGCCCTTGCACCTGACAGCCCTTACCAAGAAAGAACAGGGGAA 1345
QY 1141 GCATTAAGCAGTCAAGACTAAGTTTAAAGAGAGAGTGGCTAGAGCCCGAGGGG 1200
DB 1346 GCATTAAGCAGTCAAGACTAAGTTTAAAGAGAGAGTGGCTAGAGCCCGAGGGG 1405
QY 1201 CAGAGTATTAAGAGCGCAAGGCTCAGTAGGTGACAGAGGTTCCCAAGCAACGACATC 1260
DB 1406 CAGAGTATTAAGAGCGCAAGGCTCAGTAGGTGACAGAGGTTCCCAAGCAACGACATC 1465
QY 1261 ACAGCGAGGCAAGTCCACCAAGAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGC 1320

1466 ACAGCCGAGGAGTCCCAACAAAGTGCAAGAGCTGGAGCTTCAACGACCCGAC 1525
1321 TTCGGGCGCTCGCTGCGCCCTCAAAAGTTCTCAGCCAAACCAAGTGAATGCTGACCA 1380
1526 TTCGGGCGCTCGCTGCGCCCTCAAAAGTTCTCAGCCAAACCAAGTGAATGCTGACCA 1585
1381 GCCCTTGAGCACTGATGATATATATGATGATAAAAGATGCCAGTGTGATGATGAGAA 1440
1586 GCCCTTGAGCACTGATGATATATATGATGATAAAAGATGCCAGTGTGATGATGAGAA 1645
1441 GACCTCAACCCCACTTAAACCTGTCATTGAGCTATCAGAAATTATGAAATTTTCATGTT 1500
1646 GACCTCAACCCCACTTAAACCTGTCATTGAGCTATCAGAAATTATGAAATTTTCATGTT 1705
1501 GCAAAACGGAAGTTTAAAGAAACATTCACCTCATTATGATGATAAAGATGTCATTGAA 1560
1706 GCAAAACGGAAGTTTAAAGAAACATTCACCTCATTATGATGATAAAGATGTCATTGAA 1765
1561 TATCTGCTGCTGATCTGACATGTTGTGATGAAATTTAAAGCCTTCAACACGCTTGAT 1620
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1826 CAATTTCTTGAAAAAGGCAAAATCATCATGATTAAGAAAGCCGAGAAATTAAGACA 1885
1681 GAACATGAGACCAACACCACTTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
1886 GAACATGAGACCAACACCACTTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1945
1741 GTACAGTCCATAGATTCAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1946 GTACAGTCCATAGATTCAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2005
1801 AAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
2006 AAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2065
1861 CAGACATCTGACATCAAAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
2066 CAGACATCTGACATCAAAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2125
1921 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
2126 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2185
1981 AGCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
2186 AGCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2245
2041 GCAACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
2246 GCAACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2305
2101 GCAACACAAATAATATAGGCAACCAAGCCGAGCCCAACCAATTTAAGATGCCACCT 2160
2306 GCAACACAAATAATATAGGCAACCAAGCCGAGCCCAACCAATTTAAGATGCCACCT 2365
2161 CCTCTCCAGCCATCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2366 CCTCTCCAGCCATCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2425
2221 TTACAGAGAAAGCAATTTCTGACGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2426 TTACAGAGAAAGCAATTTCTGACGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2485
2281 GTTGCAAGTCAATCTCAACCAAGACCGTTCTATGAGGAAAGCTTTGACATGAGAGGA 2340
2486 GTTGCAAGTCAATCTCAACCAAGACCGTTCTATGAGGAAAGCTTTGACATGAGAGGA 2545
2341 GAAATCTGTGTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400

2546 GAAATCTGTGTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605
2401 CAAACCTGATCAGTGTGACCCGAGAACTGAAATATCACTTTACAGAGTGAATGCTGAACT 2460
2606 CAAACCTGATCAGTGTGACCCGAGAACTGAAATATCACTTTACAGAGTGAATGCTGAACT 2665
2461 GGCTCCAGAGGCGCCCAAGATTTTACCCCAATGGAAGGAAATCCAAATGTTTATTAAGT 2520
2666 GGCTCCAGAGGCGCCCAAGATTTTACCCCAATGGAAGGAAATCCAAATGTTTATTAAGT 2725
2521 GATGAAGAGTGGGTCCGAGAGACAGACAGACACATTTGATGATGCGGACCGACGCT 2580
2726 GATGAAGAGTGGGTCCGAGAGACAGACAGACACATTTGATGATGCGGACCGACGCT 2785
2581 GCCAGGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
2786 GCCAGGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2845
2641 AGCATTTGTAAGGACAGAGAAAGTACAGATGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 2700
2846 AGCATTTGTAAGGACAGAGAAAGTACAGATGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 2905
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2906 TAAGTCTTCATTTCTTCCAGGACATGACATGCTTTAGCCATACATATCATGATGATGA 2965
2761 ACTATTTGAAAGCCCTTTTAAAGTGAATTTGCAAAATTCGGGAAACATGAAAG 2820
2966 ACTATTTGAAAGCCCTTTTAAAGTGAATTTGCAAAATTCGGGAAACATGAAAG 3025
2821 CAGTTATTAAGCCCGTTACCTTTTAAATGATGAAATGATGATGATGATGATGATGATGATG 2880
3026 CAGTTATTAAGCCCGTTACCTTTTAAATGATGAAATGATGATGATGATGATGATGATGATG 3074

RESULT 6
US-10-399-489A-5
; Sequence 5, Application US/10399489A
; Publication No. US20050101004A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: ARGENTIERI, Thomas M.
; APPLICANT: SHELDON, Jeffrey H.
; TITLE OF INVENTION: METHODS OF SELECTING COMPOUNDS FOR MODULATION OF BLADDER FUNCTION
; FILE REFERENCE: AM100620
; CURRENT APPLICATION NUMBER: US/10/399,489A
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/241,078
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/US01/32371
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/281,428
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-489A-5

Query Match 93.0%; Score 2857.4; DB 21; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

1 GGCAGCGGATGAGAGATGTGAGTGGGCGGAGGCGAGGCTGCTGAACTGGCAGCC 60
206 GGCAGCGGATGAGAGATGTGAGTGGGCGGAGGCGAGGCTGCTGAACTGGCAGCC 265
61 GGCAGGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
266 GGCAGGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325

QY 121 GGTGGCCTTAGAGGAGACCGCCGCGGCGCAAGCAAGGGGCGCCGAGTAGAGCTGTGGGGAAG 180
Db 326 GGTGGCCTTAGAGGAGACCGCCGCGGCGCAAGCAAGGGGCGCCGAGTAGAGCTGTGGGGAAG 385
QY 181 CCGCTCTTTTACACGAGTAGCCGAGACTGCGCGCGCAAGCTCAAGTACCGGCGGGTGCAG 240
Db 386 CGCTCTCTTTACACGAGTAGCCGAGACTGCGCGCGCAAGCTCAAGTACCGGCGGGTGCAG 445
QY 241 AACTACCTGTACACGCTGTGAGAGACCCGCGGCTGGGCGTTTCACTTACCAAGCTTTC 300
Db 446 AACTACCTGTACACGCTGTGAGAGACCCGCGGCTGGGCGTTTCACTTACCAAGCTTTC 505
QY 301 GTTTTCTCTCTGTCTTTGGTCTGTTGATTTTGTCAAGTGTTCACATCCCTGAGCAC 360
Db 506 GTTTTCTCTCTGTCTTTGGTCTGTTGATTTTGTCAAGTGTTCACATCCCTGAGCAC 565
QY 361 ACAAAATGGCCCTCAAGTTGCCCTTGCATTCCTGGAATTCGTATGATTTGTGCTTTGGT 420
Db 566 ACAAAATGGCCCTCAAGTTGCCCTTGCATTCCTGGAATTCGTATGATTTGTGCTTTGGT 625
QY 421 TTGGAGTTGATCATTCGAAATCTGATCTGGGGTTCGTTTGCATATAGAGATGGCAA 480
Db 626 TTGGAGTTGATCATTCGAAATCTGATCTGGGGTTCGTTTGCATATAGAGATGGCAA 685
QY 481 GGAAGACTGAGGTTTCTCGAAAAGCCCTTCTGTGTATAGATACATTTGTTTATCGCT 540
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QY 541 TCAATAGCAGTTGTTCTGCAAAAACCTCAAGGGTATATTTTGGCCAGCTGACACTACA 600
Db 746 TCAATAGCAGTTGTTCTGCAAAAACCTCAAGGGTATATTTTGGCCAGCTGACACTACA 805
QY 601 AGTCTCCGTTTCTTACAGATCTCTCCGATGTGCGCATGGAACGAGGGGAGCACTTGG 660
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QY 781 AAAGAGTTTTCATCATATGAGATGCTCTCTGGTGGGCACAATTAATTTGACAACTAAT 840
Db 986 AAAGAGTTTTCATCATATGAGATGCTCTCTGGTGGGCACAATTAATTTGACAACTAAT 1045
QY 841 GGCCTATGAGACAAAATCCCTTAATTTGGCTGGGAAGATTGCTTCTGCAAGCTTTTGA 900
Db 1046 GGCCTATGAGACAAAATCCCTTAATTTGGCTGGGAAGATTGCTTCTGCAAGCTTTTGA 1105
QY 901 CTCCTTGGGATTTCTTCTTTTGGCACTTCGCGCGGCAATCTTGGGCTCAGGTTTGGATTA 960
Db 1106 CTCCTTGGGATTTCTTCTTTTGGCACTTCGCGCGGCAATCTTGGGCTCAGGTTTGGATTA 1165
QY 961 AAAGTACAAAGAACAAACACCGCCAGAAAACCTTTGAGAAAAGAAAGAACCCAGCTGCCAAC 1020
Db 1166 AAAGTACAAAGAACAAACACCGCCAGAAAACCTTTGAGAAAAGAAAGAACCCAGCTGCCAAC 1225
QY 1021 CTCATTTCAAGTGTGTTTGGCGTATGAGAGCTGATGAGAAATCTGTTTCCATTGCAACC 1080
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QY 1081 TGAAGCCCACTTGAAGGCTTGGACACCTGACGCTTACCAAGAAAGAAACAAGGGGGA 1140
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QY 1141 GGATCAAGCAGTCAGAAAGTAAAGTTTAAAGACGAGTGCAGATGGCTGACCCAGGGGC 1200
Db 1346 GGATCAAGCAGTCAGAAAGTAAAGTTTAAAGACGAGTGCAGATGGCTGACCCAGGGGC 1405
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Db 1406 CAGAGTATTAAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCAAGCACCGACATC 1465
QY 1261 ACAGCCGAGGGGAGTCCTCCACCAAAAGTGCAGAAAGACTGAGCTTCAAGACCGAACCCGC 1320
Db 1466 ACAGCCGAGGGGAGTCCTCCACCAAAAGTGCAGAAAGACTGAGCTTCAAGACCGAACCCGC 1525
QY 1321 TTCCGGCCCTCGCTGCGCTCAAAAAGTTCTCAGCCCAAAACAGTATAGATGTGACACA 1380
Db 1526 TTCCGGCCCTCGCTGCGCTCAAAAAGTTCTCAGCCCAAAACAGTATAGATGTGACACA 1585
QY 1381 GCCCTTGGCATGATGATGATATGATGAAAAAGATGCCAGTGTGATGATCACTGGAA 1440
Db 1586 GCCCTTGGCATGATGATGATGATGAAAAAGATGCCAGTGTGATGATCACTGGAA 1645
QY 1441 GACCTCACCCCAACCACTTAAACGTCACTTGGAGCTATCAGAAATTAAGAAATTTGATGT 1500
Db 1646 GACCTCACCCCAACCACTTAAACGTCACTTGGAGCTATCAGAAATTAAGAAATTTGATGT 1705
QY 1501 GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGTAAAGATGTCAATGAACA 1560
Db 1706 GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGTAAAGATGTCAATGAACA 1765
QY 1561 TATTCTGCTGGTCATCTGGAATGTTGTGTAGATTTAAAGCTTCAAAACGTTTGAT 1620
Db 1766 TATTCTGCTGGTCATCTGGAATGTTGTGTAGATTTAAAGCTTCAAAACGTTTGAT 1825
QY 1621 CAAATTTCTGGAAAAGGGCAATCAATCAGATTAAGAGACCGAGAAAAATTAACAGA 1680
Db 1826 CAAATTTCTGGAAAAGGGCAATCAATCAGATTAAGAGACCGAGAAAAATTAACAGA 1885
QY 1681 GAAATGAGACCAACAGACATCTCAGATGCTCGGTGCGGTGTCAAGTTGAAAAACAG 1740
Db 1886 GAAATGAGACCAACAGACATCTCAGATGCTCGGTGCGGTGTCAAGTTGAAAAACAG 1945
QY 1741 GTACAGTCCATAGAAATCCAGCTGACCTGCTACTAGACATCTATCAACAGGTCCTTGG 1800
Db 1946 GTACAGTCCATAGAAATCCAGCTGACCTGCTACTAGACATCTATCAACAGGTCCTTGG 2005
QY 1801 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCGCCACCTTTGAAATGTGA 1860
Db 2006 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCGCCACCTTTGAAATGTGA 2065
QY 1861 CAGACATCTGATTAACAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCCGCAAAAAC 1920
Db 2066 CAGACATCTGATTAACAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCCGCAAAAAC 2125
QY 1921 AGTGGCTGCTTATCCAGATCAACTTAGTGCACCAATCTGGAAGGCTTGCAGTTCTGT 1980
Db 2126 AGTGGCTGCTTATCCAGATCAACTTAGTGCACCAATCTTGAAGGCTTGCAGTTCTGT 2185
QY 1981 ACGCAAAATGAGTTCAAGTGCACCACTTCTACGCGCTTACCCCTACATGACAGTCAA 2040
Db 2186 ACGCAAAATGAGTTCAAGTGCACCACTTCTACGCGCTTACCCCTACATGACAGTCAA 2245
QY 2041 GCAACACAGGTGCCAATTAATCAAGCGATGCTCAGCAGTGGACCCACCAACCACTT 2100
Db 2246 GCAACACAGGTGCCAATTAATCAAGCGATGCTCAGCAGTGGACCCACCAACCACTT 2305
QY 2101 GCAAAACCAATTAATTAAGGACCCCAAGCCAGACGCCCAACAATTTTACATCCCACTT 2160
Db 2306 GCAAAACCAATTAATTAAGGACCCCAAGCCAGACGCCCAACAATTTTACATCCCACTT 2365
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QY 2221 TTACAGAAAGCAATTTTGAAGTCAACCACTGCTTGTGCTTCAAGAAATGTTGAG 2280
Db 2426 TTACAGAAAGCAATTTTGAAGTCAACCACTGCTTGTGCTTCAAGAAATGTTGAG 2485
QY 2281 GTTGCACAGTCAAAATTTCAACCAAGACCGTTCTATAGAGAAAGCTTTGAATGGAGAGA 2340

Db 2486 GTTGCACAGTCMAATCTCACCAAGAACCGTTTATGAGAAAGCTTTGACATGGAGGA 2545
Qy 2341 GAAACTGTGTGTCTGTCTGTCCATGTGCGCAAGAACTTGGGCAAACTTTGTCTGTG 2400
Db 2546 GAAACTGTGTGTCTGTCTGTCCATGTGCGCAAGAACTTGGGCAAACTTTGTCTGTG 2605
Qy 2401 CAAAACCTGATCAGTGTGACCGAGAACTGAAATATACACTTTTCAGGAGTGAAGTCAAGT 2460
Db 2606 CAAAACCTGATCAGTGTGACCGAGAACTGAAATATACACTTTTCAGGAGTGAAGTCAAGT 2665
Qy 2461 GGCTCCAGAGCGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTAACT 2520
Db 2666 GGCTCCAGAGCGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTAACT 2725
Qy 2521 GATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTATGCGGACCGCAAGCT 2580
Db 2726 GATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTATGCGGACCGCAAGCT 2785
Qy 2581 GCCAGGGAAGCTGCTTTGATCAGACTCTCTAAGACCTGGAAGTTCAGATCATCTCAG 2640
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Db 2846 AGCATTTGTAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAAA 2905
Qy 2701 TAAGTCTTCATTTCTTTCAGAGCAATGAGATTTTACCAATATCATTTGATGA 2760
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Qy 2761 ACTATTTGCAAGACCCCTTCTAAGAGTTGAATGCAAGATCGGGAAGAACATGAAGG 2820
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Qy 2821 CAGTTATAAGCCCGTTACTTTTAATGTGATGAATAATGATGTTTAAAG 2869
Db 3026 CAGTTATAAGCCCGTTACTTTTAATGTGATGAATAATGATGTTTAAAG 3074

RESULT 7
US-10-482-834A-55
; Sequence 55, Application US/10482834A
; Publication No.: US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Ann
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Biomomix Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 55
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-55

Query Match 93.0%; Score 2855.8; DB 21; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2860; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGCAGGCGATGAAGATGTGAGTGGGCGCGGAGAGGTGTGCTTGAATCTGGACGCC 60
Db 206 GGCAGGCGATGAAGATGTGAGTGGGCGCGGAGAGGTGTGCTTGAATCTGGACGCC 265

Qy 61 GCCAGGGGCGACGGCGCTGCTACTGTGGGCAACCGGCGGCGCACGCTTGATGGCGGCGC 120
Db 266 GCCAGGGGCGACGGCGCTGCTACTGTGGGCAACCGGCGGCGCACGCTTGATGGCGGCGC 325
Qy 121 GGTGGCTTGAAGAGAGCGCGCGGGGCAAGCAGAGGGGCGCGGATGAGCCTGTGGGGAAG 180
Db 326 GGTGGCTTGAAGAGAGCGCGCGGGGCAAGCAGAGGGGCGCGGATGAGCCTGTGGGGAAG 385
Qy 181 CCGCTCTTAAACGAGTATGCGAGAGCTGCGCGGCAAGTCAAGTACCGGCGGGTGCAG 240
Db 386 CCGCTCTTAAACGAGTATGCGAGAGCTGCGCGGCAAGTCAAGTACCGGCGGGTGCAG 445
Qy 241 AACTACCTGTACCAACCTGTGAGAGAACCCCGGCGCTGGGCGTTCACTACACGCTTTC 300
Db 446 AACTACCTGTACCAACCTGTGAGAGAACCCCGGCGCTGGGCGTTCACTACACGCTTTC 505
Qy 301 GTTTTCTCCTTGTCTTTGGTGTGATTTGTCAAGTGTTCATCAATCCCTGAGCAC 360
Db 506 GTTTTCTCCTTGTCTTTGGTGTGATTTGTCAAGTGTTCATCAATCCCTGAGCAC 565
Qy 361 ACAAAATGGCCCTCAAGTTGCCCTTGTATCCGAGATTCGTATGAATTTGTCGTTTGGT 420
Db 566 ACAAAATGGCCCTCAAGTTGCCCTTGTATCCGAGATTCGTATGAATTTGTCGTTTGGT 625
Qy 421 TTGAGATTGATCATTCGAATCTGTCTGCGGGTGTGCTTGTGATATAGAGATGGCAA 480
Db 626 TTGAGATTGATCATTCGAATCTGTCTGCGGGTGTGCTTGTGATATAGAGATGGCAA 685
Qy 481 GGAAGA CTGAGGTTGCTGGAAGCCCTTCTGTGTTATAGATACATTTCTTATCGCT 540
Db 686 GGAAGA CTGAGGTTGCTGGAAGCCCTTCTGTGTTATAGATACATTTCTTATCGCT 745
Qy 541 TCAATGCAAGTTGTTCTGCAAAAACCTCAGGGTAATATTTTGGCAAGCTGCACTGACA 600
Db 746 TCAATGCAAGTTGTTCTGCAAAAACCTCAGGGTAATATTTTGGCAAGCTGCACTGACA 805
Qy 601 AGCTCCGTTTCTACAGATCTCCGATGATGCGCATGAGACGGAAGGAGGACCTTGG 660
Db 806 AGCTCCGTTTCTACAGATCTCCGATGATGCGCATGAGACGGAAGGAGGACCTTGG 865
Qy 661 AAATTA CTGGGTTCAAGTGTATATGCTCAACAGAAAGAAATTAATCAACCTTGTGATATA 720
Db 866 AAATTA CTGGGTTCAAGTGTATATGCTCAACAGAAAGAAATTAATCAACCTTGTGATATA 925
Qy 721 GGAATTTGGTCTTAATTTTTCGCTTCCCTGTGCTATCTGTGGAAGAAAGATGCAT 780
Db 926 GGAATTTGGTCTTAATTTTTCGCTTCCCTGTGCTATCTGTGGAAGAAAGATGCAT 985
Qy 781 AAAGAGTTTCTACATATGCAATGCTCTGTGGGGGACAAATTAATTAATCACTTGAACATAT 840
Db 986 AAAGAGTTTCTACATATGCAATGCTCTGTGGGGGACAAATTAATTAATCACTTGAACATAT 1045
Qy 841 GGCATGAGACAAAACCTCCCTTAACTTGGCTGGGAAGATTTCTTTCAGAGCTTTTGA 900
Db 1046 GGCATGAGACAAAACCTCCCTTAACTTGGCTGGGAAGATTTCTTTCAGAGCTTTTGA 1105
Qy 901 CTCCTTGGATTTCTTCTTTCGACATCTCTGCGGCGCATTTCTGGCTCAGTGTTCATTA 960
Db 1106 CTCCTTGGATTTCTTCTTTCGACATCTCTGCGGCGCATTTCTGGCTCAGTGTTCATTA 1165
Qy 961 AAAGTAAAGAACACACCGCAGAAACACTTTGAGAAAGAAAGAAACCACTGCGCAAC 1020
Db 1166 AAAGTAAAGAACACACCGCAGAAACACTTTGAGAAAGAAAGAAACCACTGCGCAAC 1225
Qy 1021 CTCATTCAGTGTGTTGGGATGATTCAGAGCTGATGAGAAATCTGTTTCAATTGCAACC 1080
Db 1226 CTCATTCAGTGTGTTGGGATGATTCAGAGCTGATGAGAAATCTGTTTCAATTGCAACC 1285
Qy 1081 TGGAGGCCAACAATTGAAGGCTTTCGACACCTGCAACCCCTTACCAAAAGAAACAAAGGGAA 1140
Db 1286 TGGAGGCCAACAATTGAAGGCTTTCGACACCTGCAACCCCTTACCAAAAGAAACAAAGGGAA 1345
Qy 1141 GCATCAAGCAGTCAGAAAGCTAAGTTTAAAGAGCAGATGCCATGGCTAGCCCGAGGGGC 1200

1346 GATCAAGAGTCAAGCTAAAGTTTAAAGACGAGTGGCATGGCTAGCCCGACGGGC 1405
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1406 CAGAGATTAAAGCCGACAAAGCTCAGTAGTGAAGAGGTCGCCAAGACCCGACATC 1465
1261 ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACGACCGACCCG 1320
1466 ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACGACCGACCCG 1525
1321 TTCGGGCGCTCGTGCGCTCAAAAGTTCTCAGCCAAAACAGTGAATGATGCTGACAC 1380
1526 TTCGGGCGCTCGTGCGCTCAAAAGTTCTCAGCCAAAACAGTGAATGATGCTGACAC 1585
1381 GCGCTTGAGCATGATGATATATGATGAAGAAAGTGCAGTGAATGATGATGAGGAA 1440
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1441 GACCTCACCCCAACCACTTAACCTGTCATTCAGATCAGAAATTAAGAAATTTCACTT 1500
1646 GACCTCACCCCAACCACTTAACCTGTCATTCAGATCAGAAATTAAGAAATTTCACTT 1705
1501 GCAAAACGGAAGTTTAAAGAAACCTTAAGTCCATGATGATGAAGATGTCATTTGACAA 1560
1706 GCAAAACGGAAGTTTAAAGAAACCTTAAGTCCATGATGATGAAGATGTCATTTGACAA 1765
1561 TATTCGCTGGTCACTGGAATGATGTTGATGAATTAAGACCTTCAAAACAGTGTGAT 1620
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1826 CAAATTCCTGGAAGAGGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCA 1885
1681 GAACATGAAGACCAAGACCATCTCAGTATGCTCGTGGGTGTCAGGTTGAAAAACAG 1740
1886 GAACATGAAGACCAAGACCATCTCAGTATGCTCGTGGGTGTCAGGTTGAAAAACAG 1945
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2126 AGTGGCTGCTTACAGATCAACTAGTGAACATCTCGAGAGGCTGAGGTTCACTTGG 2185
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2186 AGCCCAATGAGTTGAGTCCGACCACTTTCTAGCGCTTACGCTTCTAGCAAGTCAA 2245
2041 GCAACACAGTGGCAATTAAGTCAAAAGCATGGTCAAGAGTGGCAAGCAACCACTT 2100
2246 GCAACACAGTGGCAATTAAGTCAAAAGCATGGTCAAGAGTGGCAAGCAACCACTT 2305
2101 GCAACCAATTAATTAAGGCAACCAAGCAAGAGCCCAACCACTTAAAGATCCCACTT 2160
2306 GCAACCAATTAATTAAGGCAACCAAGCAAGAGCCCAACCACTTAAAGATCCCACTT 2365
2161 CCTCTCCAGCATCAAGCATCTGCCAGGCAAAACTCTGCAACCTTACCTGAGGC 2220
2366 CCTCTCCAGCATCAAGCATCTGCCAGGCAAAACTCTGCAACCTTACCTGAGGC 2425
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2426 TTACAGAAAGCATTTCTGACGTCAACCACTGCTTGTGCTTCCAGAAATGTTGCG 2485
2281 GTTGACAGTCAAAATCTGACCAAGGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGA 2340
2486 GTTGACAGTCAAAATCTGACCAAGGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGA 2545
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2606 CAAAACCTGATCAGTCCAGCAAGAACTGAATATACAACTTTGAGGAGTGAAGTCAAGT 2665
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2726 GATGAAGAGTGGGTCCGGAAGAGACAGACACACTTTGATGTCGACCGACCGCT 2785
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2786 GCGAGGGAAGCTGCTTTGATCAGATCTCTGAGGACCTGGAAGGTCAGATCACTGAG 2845
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3026 CAGTTTATAGCCCGTTACTTTTATTTGATGAGAAATGATGTTTAAAG 3074

RESULT 8
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US2002040000A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KNO5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 87.6%; Score 2690.4; DB 9; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 1 ATGAAAGATGTGAGTCGGGCGGGGAGGTCGTGTGAATCTCGCAGCGCCAGGGGC 60
Qy 70 GACGGCTGTACTGCTGGGACCCGCGGGCCAGCCTTGAGCGGGCGGTGGCTG 129
Db 61 GACGGCTGTACTGCTGGGACCCGCGGGCCAGCCTTGAGCGGGCGGTGGCTG 120
Qy 130 AGGAGAGCGCGGGGCAAGCAGAGGGGGCCCGATGAGCTGTGGGAAAGCCGCTCT 189
Db 121 AGGAGAGCGCGGGGCAAGCAGAGGGGGCCCGATGAGCTGTGGGAAAGCCGCTCT 180
Qy 190 TACACGATGAGCCAGAGCTGCCGCGCAAGTCAAGTACCGGCGGTGCAAACTACCT 249
Db 181 TACACGATGAGCCAGAGCTGCCGCGCAAGTCAAGTACCGGCGGTGCAAACTACCT 240
Qy 250 TACAAGCTGTGAGAGACCCGCGGGCGGTCACTACCAAGCTTTCGTTTTCTC 309
Db 241 TACAAGCTGTGAGAGACCCGCGGGCGGTCACTACCAAGCTTTCGTTTTCTC 300
Qy 310 CTGTGCTTGGTGTGATTTGTAGTGTCTTACCATCCCTGAGCACAATAATG 369
Db 301 CTGTGCTTGGTGTGATTTGTAGTGTCTTACCATCCCTGAGCACAATAATG 360
Qy 370 GCGTCAAGTTGCTTGTATCTGAGTTCGTATGATGTGCTTGGTTGAGTTT 429
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Qy 430 ATCATTGCAATCTGCTGTGGGGTGTGTTGCAATATAGAGATGAGCAAGAACTG 489
Db 421 ATCATTGCAATCTGCTGTGGGGTGTGTTGCAATATAGAGATGAGCAAGAACTG 480
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Qy 610 TTCCTACAGATCCTCGGCAATGTCGCAATGACCAAGGGGAGGCACTTGGAAATTA 669
Db 601 TTCCTACAGATCCTCGGCAATGTCGCAATGACCAAGGGGAGGCACTTGGAAATTA 660
Qy 670 GGTTCAAGTGTATGCTCAACAGAAATTAATCAAGCTTGTATATAGATTTTGG 729
Db 661 GGTTCAAGTGTATGCTCAACAGAAATTAATCAAGCTTGTATATAGATTTTGG 720
Qy 730 GTTCTTATTTTTCGTCCTTCTGTCTATCTGTGGAAGAAAGATGCCAATAAGATT 789
Db 721 GTTCTTATTTTTCGTCCTTCTGTCTATCTGTGGAAGAAAGATGCCAATAAGATT 780
Qy 790 TCTACATATGCAATGCTCTGTGTGGGGCAATTAATTAATTAATGCTATGGA 849
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Qy 850 GACAAAACCTCCCTTAACCTGGGAGGAAATGCTTTCGAGGCTTGGACCTCTGGG 909
Db 841 GACAAAACCTCCCTTAACCTGGGAGGAAATGCTTTCGAGGCTTGGACCTCTGGG 900
Qy 910 ATTTCTTTCTTTGACATTCCTGCGGCATTTCTGGCTCAGGTTTTCATTAAGTACA 969
Db 901 ATTTCTTTCTTTGACATTCCTGCGGCATTTCTGGCTCAGGTTTTCATTAAGTACA 960
Qy 970 GAACAAACCCGCGCAAACTTTGAGAAAAGAAAGAACCCAGCTGCAACCTCATTCAG 1029
Db 961 GAACAAACCCGCGCAAACTTTGAGAAAAGAAAGAACCCAGCTGCAACCTCATTCAG 1020
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Db 1081 CACTTAAGGCTTGCACACTGCAAGCCCTTACCAAGAAAGAACAGGGAGCATCAAG 1140
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Db 1141 AGTCAGAACTTAAGTTTAAAGAGCAGATGCGCATGCGTACGCCCGAGGGCCAGATATT 1200
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Db 1261 GGCAGTCCCAACCAAGTGCAGAAAGAGCTGAGCTTCAAGACCGAAACCCGCTTCCGGCCC 1320
Qy 1330 TCGCTGCGCTCAAAAGTTCTCAGCCCAAAACAGTATGATGCTGACACAGCCCTTGGC 1389
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Qy 1390 ACTGATGATGATATGATGAAAAAGAGATCCAGTGTATGATGATGAGAGACCTCAAC 1449
Db 1381 ACTGATGATGATATGATGAAAAAGAGATCCAGTGTATGATGATGAGAGACCTCAAC 1440
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Db 1441 CCACCACTTAAAACTGTCAATTGAGCTATCAGAAATTAATGAATTTGATGCAAAACGG 1500
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Db 1621 GGAHAAGGCAATATCATCATGATTAAGAAAGCCGAGAGAAATTAACAGACATGAG 1680
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Qy 1750 ATGAATCCAGCTGACCTGACTACCTATGACATCTATCAACAGGCTCTTGGAAAGGCTCT 1809
Db 1741 ATGAATCCAGCTGACCTGACTACCTATGACATCTATCAACAGGCTCTTGGAAAGGCTCT 1800
Qy 1810 GCGTCAGCCCTGCTTGGCTTCAATTCAGTTCACACTTTTGAATGTAACAGATCT 1869
Db 1801 GCGTCAGCCCTGCTTGGCTTCAATTCAGATTCACACTTTTGAATGTAACAGATCT 1860
Qy 1870 GACTATCAAGCCCTGTGATGCAAGATCTTTCGGGTCCGCAAAACAGTGTGCTG 1929
Db 1861 GACTATCAAGCCCTGTGATGCAAGATCTTTCGGGTCCGCAAAACAGTGTGCTG 1920
Qy 1930 TTATCAGATCAACTAGTCCCAACATCTGAGAGGCTGCACTTCTTGAAGCAAT 1989
Db 1921 TTATCAGATCAACTAGTCCCAACATCTGAGAGGCTGCACTTCTTGAAGCAAT 1980
Qy 1990 GAGTTCAAGTCCCAAGCTTTCAGCGGCTTACGCTTATGCAACAGTCAACACAG 2049
Db 1981 GAGTTCAAGTCCCAAGCTTTCAGCGGCTTACGCTTATGCAACAGTCAACACAG 2040
Qy 2050 GTGCCAATTAATCAAGCAAGGCTGAGAGTGGGCAACCAACCAATTCGAAACCA 2109
Db 2041 GTGCCAATTAATCAAGCAAGGCTGAGAGTGGGCAACCAACCAATTCGAAACCA 2100
Qy 2110 ATTAATACGGCAACCAAGCCAGCCCAACCAACTTTTACAGATCCACCTCTCCCA 2169
Db 2101 ATTAATACGGCAACCAAGCCAGCCCAACCAACTTTTACAGATCCACCTCTCCCA 2160
Qy 2170 GCCATCAAGCATCTGCCCAAGGCCAAGAACTGTGACACCTTACCTGACAGCTTACAGAA 2229
Db 2161 GCCATCAAGCATCTGCCCAAGGCCAAGAACTGTGACACCTTACCTGACAGCTTACAGAA 2220

QY 2230 AGCATTTCTGACGTCAACCACTGCTTGTGCTTCCAGGAAATTTTCAGGTTGCACAG 2289
DB 2221 AGCATTTCTGACGTCAACCACTGCTTGTGCTTCCAGGAAATTTTCAGGTTGCACAG 2280
QY 2290 TCATATCTCAACCAAGACCGTTTATAGAGAAAAGCTTTGACATGGAGAGAACTCTG 2349
DB 2281 TCATATCTCAACCAAGACCGTTTATAGAGAAAAGCTTTGACATGGAGAGAACTCTG 2340
QY 2350 TTGTCGTCTGTCCTTCCATGGTGGCGAAGACCTTGGGAAATCTTGTCTGTGCAAAACCTG 2409
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QY 2410 ATCAGGTGACCGAGAACTGAATATACAATTTCAGGAGTGAATCAAGTGGCTCCAGA 2469
DB 2401 ATCAGGTGACCGAGAACTGAATATACAATTTCAGGAGTGAATCAAGTGGCTCCAGA 2460
QY 2470 GGCAGCCCAAGATTTTAACTCCCAATAGAGGAAATCCAAATTGTTTAACTGATGAAG 2529
DB 2461 GGCAGCCCAAGATTTTAACTCCCAATAGAGGAAATCCAAATTGTTTAACTGATGAAG 2520
QY 2530 GTGGGTCGCGAAGACAGAGACAGACATTTTGTATGCGCGACCGAGCTGCAAGGAA 2589
DB 2521 GTGGGTCGCGAAGACAGAGACAGACATTTTGTATGCGCGACCGAGCTGCAAGGAA 2580
QY 2590 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTGAGGCAATTTGT 2649
DB 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTGAGGCAATTTGT 2640
QY 2650 AAGGCGAGAAAGTACAGATGCTTCAAGTGGCTTCAATGTCAAACTGAATTA 2703
DB 2641 AAGGCGAGAAAGTACAGATGCTTCAAGTGGCTTCAATGTCAAACTGAATTA 2694

RESULT 9

US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeggla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CBS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Query Match 87.6%; Score 2690.4; DB 9; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 ATCAAGAGTGTGAGTCCGCGCGGAGAGGTCTGTGAATCCGACACCGCCAGGGCG 69
DB 1 ATCAAGAGTGTGAGTCCGCGCGGAGAGGTCTGTGAATCCGACACCGCCAGGGCG 60
QY 70 GACGCGCTCTACTGCTGGGCAACCGCGCGGACCGCTTGTGTGGGCGGCGGTGGCTG 129
DB 61 GACGCGCTCTACTGCTGGGCAACCGCGCGGACCGCTTGTGTGGGCGGCGGTGGCTG 120

QY 130 AAGGAGACCCGCGGAGAGAGAGGAGGCCGAGATGAGCTGTGGGAAAGCCGCTCTT 189
DB 121 AAGGAGAGCCGCGGAGAGAGAGGAGGCCGAGATGAGCTGTGGGAAAGCCGCTCTT 180
QY 130 TACAGAGTACGCAAGCTTCCGCGGCAACGTCAGTACCGCGGAGTACAGTACCTG 249
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QY 250 TACAAGTGTGAGAGACCCGCGGAGTGTGATCTACACGCTTTCGTTTTTCTC 309
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Db 1321 TCGGTGGCCCTCAAAAGTTCTCAGCCCAAAACAGTGTAGATGTGACAGAGCCCTTGGC 1380
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Db 1381 ACTGATGATGATATGATGAAAAAGATGCGAGTGTATGATGAGGAGACCTCACC 1440
Qy 1450 CCACCACTTAAACTGTCTATTCAGAGTATCAAAATTAATGAATTTCAATTTGCAAAACGG 1509
Db 1441 CCACCACTTAAACTGTCTATTCAGAGTATCAAAATTAATGAATTTCAATTTGCAAAACGG 1500
Qy 1510 AAGTTTAAAGAAACRTAACGTCCATATGATGTAAAGATGCAATGTAACCAATTTCTGCT 1569
Db 1501 AAGTTTAAAGAAACGTTAACGTCCATATGATGTAAAGATGCAATGTAACCAATTTCTGCT 1560
Qy 1570 GGTCTATGAGACATGTTGTAGATTTAAAGCCTTCAAAACAGTGTGATCAAAATTTCTT 1629
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Db 1621 GGAAGAGGCAAAATCACATGATAGAGAGCCGAGAGAAATTAACAGAGAAATCATGAG 1680
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Db 1681 ACCAGAGAGATCTCACTATGCTCGTGGGTGTCAAGGTGAAAAAGAGTACAGTCC 1740
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Db 1741 ATAGAGTCCAAAGCTGAGCTGCTCACTATGAGATCTATCAAGAGCTCTTCCGAAAGGCTCT 1800
Qy 1810 GGCCTCAGCCCTCGTCTTGGCTTCAATTCAGATTCGACCTTTTGAATGTAACAGACATCT 1869
Db 1801 GGCCTCAGCCCTCGTCTTGGCTTCAATTCAGATTCGACCTTTTGAATGTAACAGACATCT 1860
Qy 1870 GACTATCAAGCCCTGTGTAGTAAAGATCTTTCGGGTTCGCGACAAACAGTGGCTGC 1929
Db 1861 GACTATCAAGCCCTGTGTAGTAAAGATCTTTCGGGTTCGCGACAAACAGTGGCTGC 1920
Qy 1930 TTATCCAGATCAACTAGTGCACATCTCGAGAGAGCTGAGATTCATTTGAGGCCCAAT 1989
Db 1921 TTATCCAGATCAACTAGTGCACATCTCGAGAGAGCTGAGATTCATTTGAGGCCCAAT 1980
Qy 1990 GAGTTCAGTCCCGAGACTTTTCTAGCGGCTTACCCCTACTATGACAGTCAAGCAACAG 2049
Db 1981 GAGTTCAGTCCCGAGACTTTTCTAGCGGCTTACCCCTACTATGACAGTCAAGCAACAG 2040
Qy 2050 GTGCGCAATTAGTCAAAAGCGATGGTCAAGAGTGGACCAACCAACATTTGCAAAACCA 2109
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Qy 2110 ATAAATACGGGACCAAGCCAGAGCCCAACAACTTTACAGATCCCACTCTCTCTCCA 2169
Db 2101 ATAAATACGGGACCAAGCCAGAGCCCAACAACTTTACAGATCCCACTCTCTCTCCA 2160
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Db 2161 GCCATCAAGATCTGCCAGGCGCAAAATCTGCAACCTTAACCTGCAAGGCTTACAGAA 2220
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Db 2221 AGCATTTCTGACGTCACCACTGCTTGTGCTTCCAAAGAAATGTTCAAGTTTGCAAG 2280
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Db 2281 TCAAACTCAACCAAGAGACCGTTCTATGAGAAAAAGCTTTGACATGGAGAGAAACTCTG 2340
Qy 2350 TTGTCTGTCTGTCCATGCTGTCGAGAGAGCTTGGGCAATCTTTGTCTGTGAAAACTTG 2409
Db 2341 TTGTCTGTCTGTCCATGCTGTCGAGAGAGCTTGGGCAATCTTTGTCTGTGAAAACTTG 2400
Qy 2410 ATCAGGTGACCGAGAGAACTGAATATACAACTTTGAGGAGTGAAGTCAAGTGGCTCAGA 2469
Db 2401 ATCAGGTGACCGAGAGAACTGAATATACAACTTTGAGGAGTGAAGTCAAGTGGCTCAGA 2460
Qy 2470 GCGAGCAAGATTTTAACTTACCCCAATGAGAGAAATCCAAATGTTTAACTGATGAAGAG 2529
Db 2461 GCGAGCAAGATTTTAACTTACCCCAATGAGAGAAATCCAAATGTTTAACTGATGAAGAG 2520
Qy 2530 GTGGGTCCGAGAGAGACAGAGACGACCTTTTGAATGCGGACCGGACCTGCAAGGAA 2589
Db 2521 GTGGGTCCGAGAGAGACAGAGACGACCTTTTGAATGCGGACCGGACCTGCAAGGAA 2580
Qy 2590 GGTGCTTTGATCACTCTCTTAAGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2649
Db 2581 GGTGCTTTGATCACTCTCTTAAGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
Qy 2650 AAGGAGAGAGAAATGACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA 2703
Db 2641 AAGGAGAGAGAAATGACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA 2694

RESULT 10
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DROBETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJANACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIEKOPF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCN05 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-948-493-1

Query Match 87.6%; Score 2690.4; DB 21; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 ATGAGAGATGTGAGATCGGGCCGAGGAGTGTGCTGAATCTCGGACGCCGAGGGGC 69
Db 1 ATGAGAGATGTGAGATCGGGCCGAGGAGTGTGCTGAATCTCGGACGCCGAGGGGC 60
Qy 70 GACGGCTGTCTACTGTGTGGGACCCGCGGGGCAAGCTTGTGGGGGGGGGGTGGCTG 129
Db 61 GACGGCTGTCTACTGTGTGGGACCCGCGGGGCAAGCTTGTGGGGGGGGGGTGGCTG 120
Qy 130 AAGGAGAGCGCGCGGGGCAAGAGGGGGCCCGGATGAGCTGTGGGGAAGCGCTCTCT 189
Db 121 AAGGAGAGCGCGCGGGGCAAGAGGGGGCCCGGATGAGCTGTGGGGAAGCGCTCTCT 180
Qy 190 TACACGAGTACCAAGAGCTGCGGGCCCAAGTCAAGTACCGGCGGTGCAAGAACTACCTG 249
Db 181 TACACGAGTACCAAGAGCTGCGGGCCCAAGTCAAGTACCGGCGGTGCAAGAACTACCTG 240
Qy 250 TACAACTGTCGAGAGACCCCGGGCTGGGGCTTCATCAACAGCTTTCGTTTCTC 309

Db 241 TACAACTGCTGAGAGAGACCCCGGCTGGCGCTTCATCTACCAAGCTTTGGTTTCTC 300
Qy 310 CTGTGCTTTGGTGGTCTGATTTTGTCAAGTCTTTCACCACTCCCTGAGACACAAATG 369
Db 301 CTGTGCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
Qy 370 GCGTCAAGTTGCTCTTGAATCTGAGATTGATGATGATGATGATGATGATGATGATGATG 429
Db 361 GCGTCAAGTTGCTCTTGAATCTGAGATTGATGATGATGATGATGATGATGATGATGATG 420
Qy 430 ATGATTCGATCTGCTGCTGCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489
Db 421 ATGATTCGATCTGCTGCTGCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 490 AGGTTGCTCGAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
Db 481 AGGTTGCTCGAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 550 GTTGTCTTGCAGAAAACCTCAGGGTAATATTTTGGCCAGCTGCTGCTGCTGCTGCTGCTG 609
Db 541 GTTGTCTTGCAGAAAACCTCAGGGTAATATTTTGGCCAGCTGCTGCTGCTGCTGCTGCTG 600
Qy 610 TTCTTAAGATCTCCGCAATGCTGCGCATGGAACCGAAGGGAGGCACTTGGAAATTAATG 669
Db 601 TTCTTAAGATCTCCGCAATGCTGCGCATGGAACCGAAGGGAGGCACTTGGAAATTAATG 660
Qy 670 GGTTCAGTGGTTAATGCTCAGACAGAGAAATTAATGACAGCTTGGTAATGAGATTTTGG 729
Db 661 GGTTCAGTGGTTAATGCTCAGACAGAGAAATTAATGACAGCTTGGTAATGAGATTTTGG 720
Qy 730 GTTCTAATTTTTCGTCTTCTCTTCTCTAATCTGCTGGAAGAGATGCCAATAAGAGTTT 789
Db 721 GTTCTAATTTTTCGTCTTCTCTTCTCTAATCTGCTGGAAGAGATGCCAATAAGAGTTT 780
Qy 790 TCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849
Db 781 TCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 850 GACAAAACCTCCCTTAATCTGAGGAGGAGATGCTTTCGACAGGCTTTCGACCTCCCTGGC 909
Db 841 GACAAAACCTCCCTTAATCTGAGGAGGAGATGCTTTCGACAGGCTTTCGACCTCCCTGGC 900
Qy 910 ATTTCTTTCTTGGACCTTCTGCGGCAATTTGGCTCAGGTTTGGCATTAAGATACAA 969
Db 901 ATTTCTTTCTTGGACCTTCTGCGGCAATTTGGCTCAGGTTTGGCATTAAGATACAA 960
Qy 970 GAAACAACCCGCGAGAAACATTTGAAAGAGAGAAACCCAGCTGCCAATCTCATTCAG 1029
Db 961 GAAACAACCCGCGAGAAACATTTGAAAGAGAGAAACCCAGCTGCCAATCTCATTCAG 1020
Qy 1030 TGTGTTTGGCGTATGTAAGCAAGCTGATGAAATCTGTTTCAATTCGCACTTGGAGCA 1089
Db 1021 TGTGTTTGGCGTATGTAAGCAAGCTGATGAAATCTGTTTCAATTCGCACTTGGAGCA 1080
Qy 1090 CACTTGAAGGCTTGGACACTTGCAGCCCTACCAAGAAAGAAACAAGGGAGACATCAAGC 1149
Db 1081 CACTTGAAGGCTTGGACACTTGCAGCCCTACCAAGAAAGAAACAAGGGAGACATCAAGC 1140
Qy 1150 AGTCAGAACTTAAGTTTAAAGAGCGAGTCCGATAGCCCTCAGGGGCGCAGATAT 1209
Db 1141 AGTCAGAACTTAAGTTTAAAGAGCGAGTCCGATAGCCCTCAGGGGCGCAGATAT 1200
Qy 1210 AAGAGCGCAAGGCTCAGTGAAGTGAAGAGGTTCCCAAGCAGCAATCAAGCCAG 1269
Db 1201 AAGAGCGCAAGGCTCAGTGAAGTGAAGAGGTTCCCAAGCAGCAATCAAGCCAG 1260
Qy 1270 GGCAGTCCCAACCAAGTGCAGAAAGTGAAGCTTCAACGACCGAATCCGCTTCCGCGCC 1329
Db 1261 GGCAGTCCCAACCAAGTGCAGAAAGTGAAGCTTCAACGACCGAATCCGCTTCCGCGCC 1320
Qy 1330 TGGCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCTTGGC 1389

Db 1321 TCGTCCGCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGC 1380
Qy 1390 ACTGATGATGATATGATGAAAGAGATCCAGTGTGATGATGATGATGATGATGATGATGAT 1449
Db 1381 ACTGATGATGATATGATGAAAGAGATCCAGTGTGATGATGATGATGATGATGATGATGAT 1440
Qy 1450 CCACACTTAAACCTGATTCGAGCTATCAGAAATTAAGAAATTCATGTTGCAAAACGG 1509
Db 1441 CCACACTTAAACCTGATTCGAGCTATCAGAAATTAAGAAATTCATGTTGCAAAACGG 1500
Qy 1510 AAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATG 1569
Db 1501 AAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATG 1560
Qy 1570 GGTTCATGGAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1629
Db 1561 GGTTCATGGAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1630 GGAAGAGGCAAAATCAGATCAGATGAAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1689
Db 1621 GGAAGAGGCAAAATCAGATCAGATGAAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1680
Qy 1690 ACCACAGACGATCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1749
Db 1681 ACCACAGACGATCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1750 ATGAAATCCAGAGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1809
Db 1741 ATGAAATCCAGAGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Qy 1810 GCTTCAGCCCTGCTGCTTGGCTTCAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1869
Db 1801 GCTTCAGCCCTGCTGCTTGGCTTCAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1860
Qy 1870 GACTATCAAAAGCCCTGCTGATGAGCAAAAGATCTTTCGAGTTCGCGCAAAACAGTGGCTGC 1929
Db 1861 GACTATCAAAAGCCCTGCTGATGAGCAAAAGATCTTTCGAGTTCGCGCAAAACAGTGGCTGC 1920
Qy 1930 TTATCCAGATCAATCAGTGGCCAACTCTCGAAGGCTGCGAGTTCAATCTGACGCGCAAT 1989
Db 1921 TTATCCAGATCAATCAGTGGCCAACTCTCGAAGGCTGCGAGTTCAATCTGACGCGCAAT 1980
Qy 1990 GAGTTCAGTGCACAGACTTTCTAGCGGCTTACGCTTATGACAGTCAAGCAACAG 2049
Db 1981 GAGTTCAGTGCACAGACTTTCTAGCGGCTTACGCTTATGACAGTCAAGCAACAG 2040
Qy 2050 GTGCCAATTAATGCAAAAGGATGCTCAGACATGAGGACCAACACATTCGCAAAACCA 2109
Db 2041 GTGCCAATTAATGCAAAAGGATGCTCAGACATGAGGACCAACACATTCGCAAAACCA 2100
Qy 2110 ATAAATACGGCACCCAGCCAGACCCCAACCACTTAACAGATCCACCTCTCCCA 2169
Db 2101 ATAAATACGGCACCCAGCCAGACCCCAACCACTTAACAGATCCACCTCTCCCA 2160
Qy 2170 GGCATCAAGCATCTGCCAGGCCAGAAACCTTGACACCTTAAACCTTGACAGAA 2229
Db 2161 GGCATCAAGCATCTGCCAGGCCAGAAACCTTGACACCTTAAACCTTGACAGAA 2220
Qy 2220 AGCATTTTGAAGTACCACTGCTTGTGCTTCCCAAGAAATGTTCAAGTTGCAAG 2289
Db 2221 AGCATTTTGAAGTACCACTGCTTGTGCTTCCCAAGAAATGTTCAAGTTGCAAG 2280
Qy 2290 TCAAAATCTCAACCAAGGACGTTCTTATGAGAAAGCTTGAATGAGGAGAAACCTG 2349
Db 2281 TCAAAATCTCAACCAAGGACGTTCTTATGAGAAAGCTTGAATGAGGAGAAACCTG 2340
Qy 2350 TTGTCTGTCTGTCCCATGCTGCCAAGGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2409
Db 2341 TTGTCTGTCTGTCCCATGCTGCCAAGGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2400
Qy 2410 ATCAGTTCGACCGAGGAATGATATTAACAATTTCAAGGAGTGAATCAAGTGCCTCCAGA 2469
Db 2401 ATCAGTTCGACCGAGGAATGATATTAACAATTTCAAGGAGTGAATCAAGTGCCTCCAGA 2460

QY 2470 GGAGAGCAAGATTTTACCACAAATGAGGGAATCCAAATGTTTAACTGATGAGAG 2529
Db 2461 GGAGAGCAAGATTTTACCACAAATGAGGGAATCCAAATGTTTAACTGATGAGAG 2520
QY 2530 GTGGGTCCTCCAG 2589
Db 2521 GTGGGTCCTCCAG 2580
QY 2590 GCTGCTCTTTCATGAG 2649
Db 2581 GCTGCTCTTTCATGAG 2640
QY 2650 AAGGAG 2703
Db 2641 AAGGAG 2694

RESULT 11
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieker, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mehler, Michael C.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ. ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Query Match 85.8%; Score 2635.4; DB 9; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

QY 1 GGCAGGCGCATGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 97 GGCAGGCGCATGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 156
QY 61 GCCAGGCGCGAG 120
Db 157 GCCAGGCGCGAG 216
QY 121 GGTGGCTGAG 180
Db 217 GGTGGCTGAG 276
QY 181 CGGCTCTTACAG 240
Db 277 CGGCTCTTACAG 336
QY 241 AACTACTGTAACAAG 300
Db 337 AACTACTGTAACAAG 396
QY 301 GTTTTCT 360
Db 397 GTTTTCT 456

QY 361 ACAAAATGGAGCTCAAGTTGCTTATGATCTGAGATGCTGATGATGATGATGATGATGAT 420
Db 457 ACAAAATGGAGCTCAAGTTGCTTATGATCTGAGATGCTGATGATGATGATGATGATGAT 516
QY 421 TTGAGTTTCAATTCGAAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 517 TTGAGTTTCAATTCGAAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
QY 481 GGAAGACTGAGAGTTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 577 GGAAGACTGAGAGTTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 636
QY 541 TCAATGAGAGTTTCTGAAAG 600
Db 637 TCAATGAGAGTTTCTGAAAG 696
QY 601 AGTCTCGTTTCTCAAGATCTCTCGAGATGATGATGATGATGATGATGATGATGATGAT 660
Db 697 AGTCTCGTTTCTCAAGATCTCTCGAGATGATGATGATGATGATGATGATGATGATGAT 756
QY 661 AAATTAATGAGTTTCAAGTTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 757 AAATTAATGAGTTTCAAGTTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 816
QY 721 GATTTTGGTTTCTTATTTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 817 GATTTTGGTTTCTTATTTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 876
QY 781 AAAGATTTTCTCAATATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 877 AAAGATTTTCTCAATATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 936
QY 841 GGTATGAG 900
Db 937 GGTATGAG 996
QY 901 CTCTTGGAGATTTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 997 CTCTTGGAGATTTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1056
QY 961 AAAGTACAG 1020
Db 1057 AAAGTACAG 1116
QY 1021 CTCATTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1117 CTCATTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176
QY 1081 TGAAGCCACACTGTAAG 1140
Db 1177 TGAAGCCACACTGTAAG 1220
QY 1141 GCATCAAGCAGTCAG 1200
Db 1221 -----TCAGAGCTAAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1269
QY 1201 CAGAGATTAAAG 1260
Db 1270 CAGAGATTAAAG 1329
QY 1261 ACAGCGAG 1320
Db 1330 ACAGCGAG 1389
QY 1321 TTCGGGCTCTGCTGAGCTCAAAAGTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
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QY 1381 GGCCTTGGAG 1440
Db 1450 GGCCTTGGAG 1509
QY 1441 GACCTTACCCCAAGCTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1500

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Db 1510 GACCTCACCCCAACCACTTAACCTGTCATTGAGCTATCAGAAATTATGAAATTTTCATGTT 1569
Qy 1501 GCAAAACGGAGTTTAAGGAAACRTTACGTCAATATGATGTAAAGATGTCATGTGAACA 1560
Db 1570 GCAAAACGGAGTTTAAGGAAACRTTATGATGTAAAGATGTCATGTGAACA 1629
Qy 1561 TATTCTGCTGTCATGTGAACATGTTGTGTAATTTAAAGCCTTCAACACGTGTGAT 1620
Db 1630 TATTCTGCTGTCATGTGAACATGTTGTGTAATTTAAAGCCTTCAACACGTGTGAT 1689
Qy 1621 CAAATTTCTTGAAAGGCAAAATCACTCAGATTAAGAAAGCCGAGAGAAATTAACACA 1680
Db 1690 CAAATTTCTTGAAAGGCAAAATCACTCAGATTAAGAAAGCCGAGAGAAATTAACACA 1749
Qy 1681 GAAATGAGACACACAGCATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAAACAG 1740
Db 1750 GAAATGAGACACACAGCATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAAACAG 1809
Qy 1741 GTACAGTCCATAGAAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG 1800
Db 1810 GTACAGTCCATAGAAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG 1869
Qy 1801 AAAGGCTTGGCTCAGACCCCTCGCTTGGCTTCACTTCCAGTCCGACCTTTGAAATGTGA 1860
Db 1870 AAAGGCTTGGCTCAGACCCCTCGCTTGGCTTCACTTCCAGTCCGACCTTTGAAATGTGA 1929
Qy 1861 CAGACATCTGATCATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAAAC 1920
Db 1930 CAGACATCTGATCATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAAAC 1989
Qy 1921 AGTGGCTGTTATCCAGATCAACTAGTGCACATCTGAGAGGCTGAGATTCTTCTG 1980
Db 1990 AGTGGCTGTTATCCAGATCAACTAGTGCACATCTGAGAGGCTGAGATTCTTCTG 2049
Qy 1981 AGCCCAATGAGTTCAGTCCCAAGACTTTCTAGGCTTAAAGCCCTAATCTATGACACTCA 2040
Db 2050 AGCCCAATGAGTTCAGTCCCAAGACTTTCTAGGCTTAAAGCCCTAATCTATGACACTCA 2109
Qy 2041 GCACACAGGTGCATTAAGTCAAGAGTGGCTCAGAGTGGGACCCCAACACCATT 2100
Db 2110 GCACACAGGTGCATTAAGTCAAGAGTGGCTCAGAGTGGGACCCCAACACCATT 2169
Qy 2101 GCACACAGGTGCATTAAGTCAAGAGTGGCTCAGAGTGGGACCCCAACACCATT 2160
Db 2170 GCACACAGGTGCATTAAGTCAAGAGTGGCTCAGAGTGGGACCCCAACACCATT 2229
Qy 2161 CCTTCTCCAGCCATCAAGCATCTGCCAGGCGCAAACTCTGACCCCTTAACCTGTAGGC 2220
Db 2230 CCTTCTCCAGCCATCAAGCATCTGCCAGGCGCAAACTCTGACCCCTTAACCTGTAGGC 2289
Qy 2221 TTACAGAGAAAGCATTTCTGACGTCACACCTGCTTGGCTTCAAGGAAATGTTTCAG 2280
Db 2290 TTACAGAGAAAGCATTTCTGACGTCACACCTGCTTGGCTTCAAGGAAATGTTTCAG 2349
Qy 2281 GTTGCAAGTCAAAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGGAGA 2340
Db 2350 GTTGCAAGTCAAAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGGAGA 2409
Qy 2341 GAAATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2410 GAAATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2469
Qy 2401 CAAACCTGATCAGTGCAGCCGAGAACTGAATATATCAACTTTCAAGGAGTGAAGTCAAGT 2460
Db 2470 CAAACCTGATCAGTGCAGCCGAGAACTGAATATATCAACTTTCAAGGAGTGAAGTCAAGT 2529
Qy 2461 GGCTCCAGAGGACGCAAGATTTTAAACCCCAATGAGGGAATCCAAATTTGTTTAACT 2520
Db 2530 GGCTCCAGAGGACGCAAGATTTTAAACCCCAATGAGGGAATCCAAATTTGTTTAACT 2589
Qy 2521 GATGAAGAGTGGTCCGAAAGACAGACACTTTTGAATGCCGACCGCAGCCT 2580
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Db 2590 GATGAAGAGTGGTCCGAAAGACAGACAGACACTTTTGAATGCCGACCGCAGCCT 2649
Qy 2581 GCCAGGAGAGTGCCTTTGATCAGACTCTCTAAGAGCTGGAAGTCAAGTCAATCTCAG 2640
Db 2650 GCCAGGAGAGTGCCTTTGATCAGACTCTCTAAGAGCTGGAAGTCAAGTCAATCTCAG 2709
Qy 2641 AGCAATTTGTAAGGACGAGAAAGTACAGATGCTCAGCTTGCCTCATGTCAAACTGAAA 2700
Db 2710 AGCAATTTGTAAGGACGAGAAAGTACAGATGCTCAGCTTGCCTCATGTCAAACTGAAA 2769
Qy 2701 TAA 2703
Db 2770 TAA 2772

RESULT 12
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803, 268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

Query Match 85.8%; Score 2635.4; DB 19; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy 1 GGCAGCGGATGAAAGATGTGAGTGGGCGGAGGAGGAGTGTGCTGAACCTCGGACGCC 60
Db 97 GGCAGCGGATGAAAGATGTGAGTGGGCGGAGGAGGAGGAGTGTGCTGAACCTCGGACGCC 156
Qy 61 GCGAGGGGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 157 GCGAGGGGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 216
Qy 121 GGTGGCTGAGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Db 217 GGTGGCTGAGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 276
Qy 181 CCGCTCTCTTAACAGAGTACGACGCTGCGGCGCAAGCTGTCAGTCCGCGGCTGAG 240
Db 277 CCGCTCTCTTAACAGAGTACGACGCTGCGGCGCAAGCTGTCAGTCCGCGGCTGAG 336
Qy 241 AACTACCTGTACACGCTGCTGAGAGACCGCGGCTGGGAGTTCATACAGCTTTC 300
Db 337 AACTACCTGTACACGCTGCTGAGAGACCGCGGCTGGGAGTTCATACAGCTTTC 396
Qy 301 GTTTTCTCTGCTTGTGTTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
Db 397 GTTTTCTCTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 456
Qy 361 ACAAATTTGGCCTCAAGTTGCTTGTATCCTGAGATTGATGATGTTGTTGTTGTTGTT 420
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Db 457 ACAAATTTGGCTCAAGTGTGCTCTTGAATCTGAGAGTTCGATGATGATGCTGCTTTGCT 516
Qy 421 TTGGAGTTTCATTCATTCGAAATCTGTCTGCGGGTTCCTGTTGTGATATAGAGATGCGAA 480
Db 517 TTGGAGTTTCATTCATTCGAAATCTGTCTGCGGGTTCCTGTTGTGATATAGAGATGCGAA 576
Qy 481 GGAAGATGAGGTTTGTCTCGAAGGCCCTTGCTGTGTTATAGATACATGTTCTTATGCT 540
Db 577 GGAAGATGAGGTTTGTCTCGAAGGCCCTTGCTGTGTTATAGATACATGTTCTTATGCT 636
Qy 541 TCAATAGCAGTGTGTTTCTGCAAAAATCTAGGGTAAATATTTTGTGCAAGTGTGACTAGA 600
Db 637 TCATAGCAGTGTGTTTCTGCAAAAATCTAGGGTAAATATTTTGTGCAAGTGTGACTAGA 696
Qy 601 AGTCTCGGTTTCTTCAAGATCTCTCGGATGCTGCGCATGAGACGAGGGAGGCACTTGG 660
Db 697 AGTCTCGGTTTCTTCAAGATCTCTCGGATGCTGCGCATGAGACGAGGGAGGCACTTGG 756
Qy 661 AAATTAAGTGGGTTTCAAGTGTGTTATGCTCAGCAAGGAATTAATCAGCTTGGTACATA 720
Db 757 AAATTAAGTGGGTTTCAAGTGTGTTATGCTCAGCAAGGAATTAATCAGCTTGGTACATA 816
Qy 721 GGAATTTTGGTCTTATTTTGTGCTCTTCTGCTATCTGATGAGTGAAGATGCGCAAT 780
Db 817 GGAATTTTGGTCTTATTTTGTGCTCTTCTGCTATCTGATGAGTGAAGATGCGCAAT 876
Qy 781 AAAGATTTTCTACATATGCAAGATGCTCTGTGCGGCAAAATTAATGACACTATTT 840
Db 877 AAAGATTTTCTACATATGCAAGATGCTCTGTGCGGCAAAATTAATGACACTATTT 936
Qy 841 GGGTATGAGACAAAATCTCCCTTAATCTGCTGGGAAATGCTTCTGAGGCTTTGCA 900
Db 937 GGGTATGAGACAAAATCTCCCTTAATCTGCTGGGAAATGCTTCTGAGGCTTTGCA 996
Qy 901 CTCCTTGGCAATTTCTTCTTGTGCACTTCTGCGGCAATCTTGGCTCAGGTTTGTGATTA 960
Db 997 CTCCTTGGCAATTTCTTCTTGTGCACTTCTGCGGCAATCTTGGCTCAGGTTTGTGATTA 1056
Qy 961 AAAGTACAGAAACAAACCGCCGCAAAACATTTGAGAAAAGAAAGAAAGAAAGAAAGAAAG 1020
Db 1057 AAAGTACAGAAACAAACCGCCGCAAAACATTTGAGAAAAGAAAGAAAGAAAGAAAGAAAG 1116
Qy 1021 CTCATTCAAGTGTGTTTGGGCTAGTTAGCGAGCTGATGAGAAATCTGTTCCATTGCAATC 1080
Db 1117 CTCATTCAAGTGTGTTTGGGCTAGTTAGCGAGCTGATGAGAAATCTGTTCCATTGCAATC 1176
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Db 1177 TGGAGCCACACTTGAAGGCTTGGCAACCTGAGGCTTACCAAGAAAGAAAGAAAGGAGAA 1220
Qy 1141 GCATCAAGCAGTGAAGGCTTGAAGGAGCGAGTGGCATGCGTACAGGCTTCCAGGAGC 1200
Db 1221 -----TCAGAGGCTTAAGTGTGTTTGAAGAGCGAGTGGCATGCGTACAGGCTTCCAGGAGC 1269
Qy 1201 CAGAGTATTAAGAGCGAGCAAGGCTCAGTAGTGAAGAGGCTCCCAAGCAACGACATC 1260
Db 1270 CAGAGTATTAAGAGCGAGCAAGGCTCAGTAGTGAAGAGGCTCCCAAGCAACGACATC 1329
Qy 1261 ACAGCGAGGAGGAGTCCACCAAAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCG 1320
Db 1330 ACAGCGAGGAGGAGTCCACCAAAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCG 1389
Qy 1321 TTCCGGCCCTGCTGGGCTCAAAAGTTCACGCCCAAAACAGTATAGATGCTGACACA 1380
Db 1390 TTCCGGCCCTGCTGGGCTCAAAAGTTCACGCCCAAAACAGTATAGATGCTGACACA 1449
Qy 1381 GGCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1450 GGCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
Qy 1441 GACCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500

Db 1510 GACCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1569
Qy 1501 GCAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGAT 1560
Db 1570 GCAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGAT 1629
Qy 1561 TATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1630 TATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1689
Qy 1621 CAAATTTCTGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
Db 1690 CAAATTTCTGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1749
Qy 1681 GAAATGAGACCAAGACGATCTCAGTATGCTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1740
Db 1750 GAAATGAGACCAAGACGATCTCAGTATGCTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1809
Qy 1741 GTACAGTCCATGAAATCCAAAGCTGAGCTGCTTACATGATGATGATGATGATGATGATGATG 1800
Db 1810 GTACAGTCCATGAAATCCAAAGCTGAGCTGCTTACATGATGATGATGATGATGATGATGATG 1869
Qy 1801 AAAGGCTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
Db 1870 AAAGGCTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1929
Qy 1861 CAGACATCTGACTATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Db 1930 CAGACATCTGACTATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1989
Qy 1921 AGTGGCTGCTTACAGATCAATGATGAGCAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1980
Db 1990 AGTGGCTGCTTACAGATCAATGATGAGCAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 2049
Qy 1981 AGGCAATGAGTTCAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
Db 2050 AGGCAATGAGTTCAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2109
Qy 2041 GCAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
Db 2110 GCAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2169
Qy 2101 GCAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
Db 2170 GCAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2229
Qy 2161 CCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
Db 2230 CCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2289
Qy 2221 TTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Db 2290 TTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2349
Qy 2281 GTTGACAGTCAAAATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
Db 2350 GTTGACAGTCAAAATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2409
Qy 2341 GAAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2400
Db 2410 GAAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2469
Qy 2401 CAAAACCTGATCAGGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2460
Db 2470 CAAAACCTGATCAGGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2529
Qy 2461 GGCCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
Db 2530 GGCCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2589
Qy 2521 GATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
Db 2590 GATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2649

QY 2581 GCCAGGGAAGCTCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGATCATCTG 2640
DB 2650 GCCAGGGAAGCTCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGATCATCTG 2709
QY 2641 AGCATTTGTAAGGACGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2700
DB 2710 AGCATTTGTAAGGACGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2769
QY 2701 TAA 2703
DB 2770 TAA 2772

RESULT 13

US-09-810-796-3
Sequence 3, Application US/09810796
Patent No. US20020102677A1
GENERAL INFORMATION:
APPLICANT: Jegla, Timothy James
APPLICANT: ICAGEN, Inc.
TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 potassium Channel
FILE REFERENCE: 018512-005010US
CURRENT APPLICATION NUMBER: US/09/810,796
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/190,954
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
NAME/KEY: CDS
LOCATION: (1)..(2667)
OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
US-09-810-796-3

Query Match 85.5%; Score 2626.4; DB 9; Length 2667;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
QY 10 ATGAAGATGTGAGTCGAGCCGAGGAGGAGTCTCTGTAAGTCCGACAGCCGACAGGAGC 69
DB 1 ATGAAGATGTGAGTCGAGCCGAGGAGGAGTCTCTGTAAGTCCGACAGCCGACAGGAGC 60
QY 70 GACGAGCTGCTACTGCTGGGACCCGCGCGGACGCTTGTGTGGCGGCGGCTGGCTTG 129
DB 61 GACGAGCTGCTACTGCTGGGACCCCGCGGACGCTTGTGTGGCGGCGGCTGGCTTG 120
QY 130 AGGAGAGCCGCGGAGGCAAGGAGGAGGCGCGGATAGAGCTGTGGGAGAACCCGCTCTT 189
DB 121 AGGAGAGCCGCGGAGGCAAGGAGGAGGCGCGGATAGAGCTGTGGGAGAACCCGCTCTT 180
QY 190 TACACAGTAGCAGAGAGTGCAGGCGCAAGCTCAAGTAACGAGGAGGTGAGAACTACTG 249
DB 181 TACACAGTAGCAGAGAGTGCAGGCGCAAGCTCAAGTAACGAGGAGGTGAGAACTACTG 240
QY 250 TACACAGTAGCAGAGAGCCCGGAGCTGGGCTTCATCAACGCTTTCGTTTTTCTC 309
DB 241 TACACAGTAGCAGAGAGCCCGGAGCTGGGCTTCATCAACGCTTTCGTTTTTCTC 300
QY 310 CTGTGCTTTGGTGTGCTGATTTTGTGAGTGTTCACATCCCTGAGACACAAATTTG 369
DB 301 CTGTGCTTTGGTGTGATTTTGTGAGTGTTCACATCCCTGAGACACAAATTTG 360
QY 370 GCCTCAAGTTGACTCTTGAATCCTGAGTTCGTGATGATTCGTCTTTGGTTGAGTTC 429
DB 361 GCCTCAAGTTGACTCTTGAATCCTGAGTTCGTGATGATTCGTCTTTGGTTGAGTTC 420

QY 430 ATCATCGAATCTGTGCTCGGAGTTGTCTGTTGCGATATTAAGAGATGCGCAAGAGACTG 489
DB 421 ATCATTCGAATCTGTGCTCGGAGTTGTCTGTTGCGATATTAAGAGATGCGCAAGAGACTG 480
QY 490 AGGTTGCTCGAAGCCCTTCTGTGTATTAAGATACATTTGTTTATTCGCTTCAATAGCA 549
DB 481 AGGTTGCTCGAAGCCCTTCTGTGTATTAAGATACATTTGTTTATTCGCTTCAATAGCA 540
QY 550 GTTGTTCGCAAAAACCTCAGGGTAAATTTTTCGACGTCGACCTCAGAAAGTCCGCT 609
DB 541 GTTGTTCGCAAAAACCTCAGGGTAAATTTTTCGACGTCGACCTCAGAAAGTCCGCT 600
QY 610 TTCTTACAGATCTCTCCGATGGTGGCAGTGAACCGAAGGAGGACCTTGGAAATTAAGT 669
DB 601 TTCTTACAGATCTCTCCGATGGTGGCAGTGAACCGAAGGAGGACCTTGGAAATTAAGT 660
QY 670 GGTTCAGTGTGTTATGCTCAGCAGAGAAATTAATCAGCTTGTGATCATAGATTTTGG 729
DB 661 GGTTCAGTGTGTTATGCTCAGCAGAGAAATTAATCAGCTTGTGATCATAGATTTTGG 720
QY 730 GTTCTTATTTTTCGTCCTTTCCTGTCATCTGCTGGAAGAAAGGATGCCAATTAAGT 789
DB 721 GTTCTTATTTTTCGTCCTTTCCTGTCATCTGCTGGAAGAAAGGATGCCAATTAAGT 780
QY 790 TCTACATATGACAGATGCTCTGTGGGCAACAATTAATGACAACTATTGGCTATGGA 849
DB 781 TCTACATATGACAGATGCTCTGTGGGCAACAATTAATGACAACTATTGGCTATGGA 840
QY 850 GACAAATCTCCCTTAACTTGGCTGGGAAGATTGCTTTCGACGCTTTCGACCTCCTTGGC 909
DB 841 GACAAATCTCCCTTAACTTGGCTGGGAAGATTGCTTTCGACGCTTTCGACCTCCTTGGC 900
QY 910 ATTCTTCTTTTGCACCTTCCTGCGGACATCTTGGCTCAGGTTTGGATTAAATAGCA 969
DB 901 ATTCTTCTTTTGCACCTTCCTGCGGACATCTTGGCTCAGGTTTGGATTAAATAGCA 960
QY 970 GAACAACACCCGACAGAAACCTTTGAGAAAGAGAAACCAAGCTCCCACTCATTCAG 1029
DB 961 GAACAACACCCGACAGAAACCTTTGAGAAAGAGAAACCAAGCTCCCACTCATTCAG 1020
QY 1030 TGTGTTTGGCGATGATTAAGGAGGAGTGAAGAAATCTGTTTCATTTGCAACCTGGAAGCA 1089
DB 1021 TGTGTTTGGCGATGATTAAGGAGGAGTGAAGAAATCTGTTTCATTTGCAACCTGGAAGCA 1080
QY 1090 CACTTGAAGGCTTTCACACCTGACGCTTCAAGAAAGAAACAAAGGGAAGCATCAAGC 1149
DB 1081 CACTTGAAGGCTTTCACACCTGACGCTTCAAGAAAGAAACCAAGGGAAGCATCAAGC 1115
QY 1150 ACTCAGAACTPAAGTTTAAAGAGCGAGTGGCATGCTAGCCCGAGGGCCAGATATT 1209
DB 1116 --TCAGAAAGCTPAAGTTTAAAGAGCGAGTGGCATGCTAGCCCGAGGGCCAGATATT 1173
QY 1210 AAGAGCGACAAAGCTCGATGATGAGAGAGTCCCAAGACCGAATCAACAGCCGAG 1269
DB 1174 AAGAGCGACAAAGCTCGATGATGAGAGAGTCCCAAGACCGAATCAACAGCCGAG 1233
QY 1270 GGCAGTCCACCAAGAGTGCAGAGAGTGAAGCTTCAACGACCGAACCCTTCCGAGCC 1329
DB 1234 GGCAGTCCACCAAGAGTGCAGAGAGTGAAGCTTCAACGACCGAACCCTTCCGAGCC 1293
QY 1330 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAAACCAAGTATGATGCTGACACAGCCTTGGC 1389
DB 1294 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAAACCAAGTATGATGCTGACACAGCCTTGGC 1353
QY 1390 ACTGATGATGATATGATGAGAAAGAGATGAGTGTGATGATGATGATGATGATGATGATGAT 1449
DB 1354 ACTGATGATGATATGATGAGAAAGAGATGAGTGTGATGATGATGATGATGATGATGATGAT 1413
QY 1450 CCACCACTTAAACCTGTCAATCGAGCTATCAGAAATTAATGAATTTCAATGTTGCAAAACGG 1509
DB 1414 CCACCACTTAAACCTGTCAATCGAGCTATCAGAAATTAATGAATTTCAATGTTGCAAAACGG 1473
QY 1510 AAGTTTAAGAAACCTTTCGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1569

Db 1474 AAGTTAAGGAAAGTACGTCATATGATGTAAGATGTCATGTAACATATTCGCT 1533
Qy 1570 GGTTCATCGACATGTTGTGTAGAAATTAAGACCTTCAACAGGTGTGATCAATTCCT 1629
Db 1534 GGTTCATCGACATGTTGTGTAGAAATTAAGACCTTCAACAGGTGTGATCAATTCCT 1593
Qy 1630 GGAAGAGGCAAAATCATCATGATGATGAAGAGCCGAGAGAAATTAACAGAGAACTAG 1689
Db 1594 GGAAGAGGCAAAATCATCATGATGATGAAGAGCCGAGAGAAATTAACAGAGAACTAG 1653
Qy 1690 ACCACAGACGATCTCACTATGCTCGGTGCGGTGCTCAAGGTTGAAAAAGTACACTCC 1749
Db 1654 ACCACAGACGATCTCACTATGCTCGGTGCGGTGCTCAAGGTTGAAAAAGTACACTCC 1713
Qy 1750 ATAGAAATCCAGATGAGCTGCTCTATGACATCTATCAACAGGTCCTCCGAAAAGCTCT 1809
Db 1714 ATAGAGTCCAGATGAGCTGCTCTATGACATCTATCAACAGGTCCTCCGAAAAGCTCT 1773
Qy 1810 GCGTCAGACCCCTCGCTTGGGCTTCATTCAGTCCACCTTTTGAATGTGAACAGACATCT 1869
Db 1774 GCGTCAGACCCCTCGCTTGGGCTTCATTCAGTCCACCTTTTGAATGTGAACAGACATCT 1833
Qy 1870 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCCGGGTTCCGCAAAAAGTGGCTGC 1929
Db 1834 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCCGGGTTCCGCAAAAAGTGGCTGC 1893
Qy 1930 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTCGAGTTCACTTTCAGAGCCCAAT 1989
Db 1894 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTCGAGTTCACTTTCAGAGCCCAAT 1953
Qy 1990 GAGTTCAGTGGCCGAGCTTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2049
Db 1954 GAGTTCAGTGGCCGAGCTTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2013
Qy 2050 GTGGCAATTAAGTCAAAAGCGATGGCTCAGAGTGGCAAGCCCAACCAACATTTGAAACCA 2109
Db 2014 GTGGCAATTAAGTCAAAAGCGATGGCTCAGAGTGGCAAGCCCAACCAACATTTGAAACCA 2073
Qy 2110 ATAAATTCGGGCAAGCCCAAGCCGACGACCCCAACATTTACAGATCCCACTCTCTCCCA 2169
Db 2074 ATAAATTCGGGCAAGCCCAAGCCGACGACCCCAACATTTACAGATCCCACTCTCTCCCA 2133
Qy 2170 GCATCAAGATCTGGCCGAGGCGCAAACTGTGACCTCAACCTGAGGCTTACAGGAA 2229
Db 2134 GCATCAAGATCTGGCCGAGGCGCAAACTGTGACCTCAACCTGAGGCTTACAGGAA 2193
Qy 2230 AGCATTTCTGACGTCACACCTGCTTGTGCTTCAAGGAAATGTTCAAGTTGCACAG 2289
Db 2194 AGCATTTCTGACGTCACACCTGCTTGTGCTTCAAGGAAATGTTCAAGTTGCACAG 2253
Qy 2290 TCAAAATTCACCAAGACCGTTCTATAGAGAAAAGCTTTGACATGGAGAGAACTCTG 2349
Db 2254 TCAAAATTCACCAAGACCGTTCTATAGAGAAAAGCTTTGACATGGAGAGAACTCTG 2313
Qy 2350 TTGTCGTCTGTCCTCCAGTGTGCGGAAAGCTTGGGCAAACTTTGTCTGTGCAAAACTG 2409
Db 2314 TTGTCGTCTGTCCTCCAGTGTGCGGAAAGCTTGGGCAAACTTTGTCTGTGCAAAACTG 2273
Qy 2410 ATCAGTTCGACCGAGAACTGAATATATCAACTTTCAAGGAGTGAAGTCAATGCTCCAGA 2469
Db 2374 ATCAGTTCGACCGAGAACTGAATATATCAACTTTCAAGGAGTGAAGTCAATGCTCCAGA 2433
Qy 2470 GGCAGCCCAAGATTTTTCACCCAAATGGAAGGATTCAAATTTGTTTATTAATGATGAAG 2529
Db 2434 GGCAGCCCAAGATTTTTCACCCAAATGGAAGGATTCAAATTTGTTTATTAATGATGAAG 2493
Qy 2530 GTGGGTCGCGAAGAGACAGACACATTTTATGTCGACCGGACCGCTCCAGGAGAA 2589
Db 2494 GTGGGTCGCGAAGAGACAGACACATTTTATGTCGACCGGACCGCTCCAGGAGAA 2553
Qy 2590 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGATCATCTCAGAGCATTTGT 2649

Db 2554 GCTGCTTTGATCAGACTCTCTAAGACTGGAAGGTCAACATCTTCAGACATTTGT 2613
Qy 2650 AAGGACAGAGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAATTA 2703
Db 2614 AAGGACAGAGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAATTA 2667

RESULT 14
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stegallano, Nancy
; APPLICANT: Perodini, Jacqueline
; APPLICANT: Rodrigue-May, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1120,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 33394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 55590, 15992, 2094, 2252, 3474,
; FILE REFERENCE: MP102-018P1RNMNIM
; CURRENT FILING DATE: 2003-01-29
; PRIOR FILING DATE: 2003-01-29
; PRIOR FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-03-15
; PRIOR FILING DATE: 2002-03-15
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-04-29
; PRIOR FILING DATE: 2002-04-29
; PRIOR FILING DATE: 2002-06-12
; PRIOR FILING DATE: 2002-06-12
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2002-07-03
; PRIOR FILING DATE: 2002-07-03
; PRIOR FILING DATE: 2002-07-10
; PRIOR FILING DATE: 2002-07-10
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 2002-08-23
; PRIOR FILING DATE: 2002-08-23
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55

Query Match 16.9%; Score 518; DB 17; Length 2335;
Best Local Similarity 60.1%; Pred. No. 2.9e-139;
Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

Qy 226 TACCGCGGGTGAGAACTACCTGTACCAAGTGTGAGAGACCCCGCGCTGGGCTTC 285
Db 320 TACCGCGGGTGAGAACTACCTGTACCAAGTGTGAGAGACCCCGCGCTGGGCTTC 379
Qy 286 ATCTACACGCTTGTGTTTCTCTGTTGCTTGTGCTTGAATTTGTCAAGTGTTCCT 345
Db 380 GTCTACACGCTTGTGTTTCTCTGTTGCTTGTGCTTGAATTTGTCAAGTGTTCCT 439

QY 346 ACCATCCCTGAGCACA CAAAATTGGCCCTCAAGTTGCTCTTGAATCCTGAGTTGCTGATG 405
Db 440 ACTATCCAGAGACACGAGAACTTGGCAACGAGTGTCTCTCATCTTGGAAATTCGTGATG 499
QY 406 ATTGTGCTCTTGGTTGGAGTTCATCATTCGAAATCTGGTCTGGGGTGGTGGTCTGATCA 465
Db 500 ATCGTGGTCTTGGCTGGAGTACATGTCGGGGTCTGGTCCGCGGATGCTGGTCCGCG 559
QY 466 TATAGAGATGCGAAGAAAGACTGAGTTGTCTGAAAAGCCCTTCTGTGTTATAGATAC 525
Db 560 TACCGAGATGAGAGGGTGTCTTCGGCTTGGCAAAAAGCCCTTCTGTGATGCACTTC 619
QY 526 ATTGTCTTATCGCTTCAATAGCATGTTGTTCTGCAAAAATCAGGGTAATATTTTGGC 585
Db 620 ATGCTTGTGCTGCTCGGTGGCCGTCAATCGCCGGGTACCCAGGGCAACATCTTCGCGC 679
QY 586 AGCTCTGCACTGAGAGTCTCGGTTCCTAAGATCTCTCCGCAATGTTGGGCAATGACCA 645
Db 680 AGCTCGCGCTGGCGAGCATGCGCTTCTGCAAGATCTTGCGCATGGTGGCATGAGCCGC 739
QY 646 AGGGAGGCACTTGAATTTACTGGGTTCAAGTGTATGCTCAAGCAAGGAATTAATC 705
Db 740 CCGGGGGGCACTGGAAGCTGCTGGGCTCAGTGTCTACGCGATAGCAAGAGCTGATC 799
QY 706 ACAGCTTGTACATAGAAATTTTGTCTTATTTTTCGTCTTCTGTCTATCTGTG 765
Db 800 ACGGCTGTGATACATCGGGTTCCTGCTGCTCATCTTGCCCTCTTCTGCTTACCTGGCC 859
QY 766 GAAAAGATGCGCAATTAAGATTTCTAATATGAGATGCTCTCGGTGGGCGCAAT 825
Db 860 GAGAAAGAGCGCACTCCGACTTCTCTCTCTACGCGACTCGTCTGGTGGGGAGAGATT 919
QY 826 ACATTGACAACTATTTGGCTATGAGACAAAATCTCCCTAATCTGGCTGGAAAGATTGCTT 885
Db 920 ACATTGACAACTATGGCTATGAGTGAACAACGCGCAACATGGTGGGAGGGGTCTG 979
QY 886 TCTGAGGCTTGGCACTCTTGGCAATTTCTTTTGTGCACTTCCTGCGGCAATTTGGC 945
Db 980 GGTGCTGGCTCTGCTTACTGAGCATCTTTCTTTTGGCCCTGCTGCGGCATCTCAGGC 1039
QY 946 TCAGTTTGGCAATTAAGATTAACAAGAACAAACCGCGCAAAAACATTTAGAAAGAAAG 1005
Db 1040 TCGGCTTTGGCCCTGAAGGTCAGAGAGACACCGCGCAAGAAAGACTTCAAGAAAGCGAAG 1099
QY 1006 AACCCGACTGCCAATCTCATTTAGTGTGTTGGCTGATTAAGCAGCTGATGAAATCT 1065
Db 1100 ATGCCGGGAGCCAACTCATTCAGAGCTGCTGGCGCTGTACTCCAGCATATGAGCCGG 1159
QY 1066 GTTTCATTGCAACTGGAAGCCACATTTGAAGGCTTGCAACCTGCAAGC----- 1116
Db 1160 GCTTACTTGACAGCCACTGTGTACTACTATGACAGTATCTCCCATCTTCAAGAGAGCTG 1219
QY 1117 CCTACCAAGAAAGAAACAAGGGGAAGCATAGACAGTCAAGAGCTA----- 1161
Db 1220 GCCCTTTTGTGAGCAGTGAACGCGGCCGCAATGGGGGCTTACGCGCCCTGAGAGTG 1279
QY 1162 ----- 1161
Db 1280 CGGCGGGCGCGGTACCGGACGGAAGCCTCCCGTTACCGCGCGTGGTCCACTGGCAC 1339
QY 1162 -----AGTTTAAAGAGCGA 1176
Db 1340 CGGCGGGGAGACCTCTTCTGCTCTGGGAAAGACCGGATGGGATCAAAAGACCGC 1399
QY 1177 GTGGCGATGGCTAGCCCGAGGGGCGAGA-----GTATTAAGAGCGCAAGACCTCAGTA 1230
Db 1400 ATCCGATGGGAGCTCCAGGCGGGGAGAGGGTCTTCAAGAGAGAGTGGCACCCTCCA 1459
QY 1231 GGTGACAGAGGTCCCAAGACACCGACATCAGAGCCGAGG---GAGTGTCCCAAGAGTG 1287
Db 1460 ACAATGCCACCTCCCAAGCAGCGAGGAGGTGGGTGAAGGCCACAGGCCCAAGAGGTG 1519

QY 1288 CAGAAAGCTGAGGCTTCAAGACCGGAACCGGCTTCCGGCCCTGCTGACCTCAAAAGT 1347
Db 1520 CAAAAGCTGGAGCTTCAATGATCCGACCCGCTTCCGGGCACTCTGTGAGACTC----- 1573
QY 1348 TCTCAGCCAAAACCAAGTATAGATGCTGACACAGCCCTTGGCACTGATGATATATGAT 1407
Db 1574 -----AAACCCCGCACTTGTGTAGAGATGCC---CCTCAGAGAAAGTATACAGAG 1621
QY 1408 GAAAAGATGCGCACTGATGATGATCACTGAGAAAGACTCACCCCACTTAAACTGTC 1467
Db 1622 GAGAAAGAGTACCAATGTGAGTCAAGGTGAGACGACATCATGCTGTGTGAAGACAGTC 1681
QY 1468 ATTGAGCTATCAGATTAATGAAATTTATGTTGCAAAAAGGATTTAAGGAAACRTTA 1527
Db 1682 ATCCGCTCATCAGGATTTCTAAGTTCTGTTGGCCAAAAGGAAATTCAGAGAGACACTG 1741
QY 1528 GGTCCATATGATGTAAAGATGTCTAATGAACAATTTGCTGCTGATCTGACATGTTG 1587
Db 1742 GAACTGTGACAGTGAAGAGCTCATTTGAGCAATCTAGACAGGCGCACCTGGACATGCTG 1801
QY 1588 TGTAGAAATTAAGGCTTCAAAACAGTGTGATCAAAATTTGGAAGAGGCG---AAATC 1644
Db 1802 GCGCGGATCAAGAGCTGCAAACTCGGTTGAGCAAAATTTGGGTGCGGGGCGCCGGGAGC 1861
QY 1645 ACATCAGATTAAGAGAGCCGAGAGAAAATTAACAGCAATGAGACACAGACATCTC 1704
Db 1862 AGGAAGGCCCGGAGAGAGGGGACAAAGGGGCTTCGACGCGAGAGTGGATGAATAATC 1921
QY 1705 AGTATGCTCGGTGGGAGGTGCAAGGTTGAAAACAGATCAAGTCAATGAAATCCAAAGCTG 1764
Db 1922 AGCATGATGAGACGCGTGTCAAGGTGGAAGAGAGTGCAGTCCATGAGACAAAGCTG 1981
QY 1765 GACTGCTACTAGACATCTATCAACAGGTCTTGGAAAGGCTGCTGACGCCCTGCT 1824
Db 1982 GACCTGCTGTTGGGCTTCTATTCGGCTGCTGC-----GCTGAGCACTCGGCGAGC 2035
QY 1825 TTGGCTTATTCAGTCTCCACCTTTGAATGTGAACAGACATGATATCAAAAGCCT 1884
Db 2036 CTGGGCGCGGTGCAAGTGCCTGCTGTCGACCCCGACATCACCTCGATCACACAGCCT 2095
QY 1885 GTGATGCAAGAAATCTTTCGGGTTCCGACAAA 1918
Db 2096 GTGACCAAGAGACATCTCCGCTTCGACACAGA 2129

RESULT 15
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850, 928
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-10-850-928-1

Query Match 16.94; Score 518; DB 21; Length 2335;

Best Local Similarity 60.1%; Pred. No. 2.9e-139;
Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

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QY 226 TACCGCGGGGTGCAGAACTACCTGTACAAAGTGTGAGAGACCCCGGCTGGGCTTC 285
Db 320 TACCGCGGGGTGCAGAACTACCTGTACAAAGTGTGAGAGACCCCGGCTGGGCTTC 379
QY 286 ATCTACACGCTTTCGTTTTCTCTGTCTTGTGGTGGTCTGAATTTTGTAGTGTTC 345
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 08:19:35 ; Search time 296.493 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2689.2	99.8	3137	4	US-09-590-304-1
2	2681.2	99.5	3074	4	US-09-813-148-1
3	2625.2	97.4	2772	4	US-09-825-147-1
4	2625.2	97.4	3111	4	US-09-825-147-3
5	518.4	19.2	2196	4	US-09-949-016-1823
6	518.4	19.2	2335	4	US-09-492-361-1
7	516	19.2	2273	3	US-09-177-650-88
8	510	18.9	2169	3	US-09-105-058C-22
9	509.8	18.9	582	4	US-09-495-050A-303
10	465.4	17.3	886	3	US-09-105-058C-1
11	464	17.2	2814	3	US-09-177-650-90
12	460.8	17.1	2565	3	US-09-105-058C-26
13	460.8	17.1	2914	3	US-09-177-650-6
14	452	16.8	575	4	US-09-495-050A-305
15	425	15.8	3287	3	US-09-105-058C-19
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ALIGNMENTS

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; Sequence 1, Application US/09590304									
; Patent No. 6649371									
; GENERAL INFORMATION:									
; APPLICANT: JENTECH, Thomas									
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN									
; FILE REFERENCE: 2815-0136P									
; CURRENT APPLICATION NUMBER: US/09/590,304									
; CURRENT FILING DATE: 2000-06-09									
; NUMBER OF SEQ ID NOS: 10									
; SOFTWARE: PatentIn version 3.0									
; SEQ ID NO 1									
; LENGTH: 3137									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (1)..(2691)									
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Matches 2691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
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OY	1201	AAGAGCCGACAGCCTCATGATGATGACAGAGGTGCCCAAGCACCCGACATCAAGCCGAG	1260
Dd	1415	AAGAGCCGACAGCCTCATGATGATGACAGAGGTGCCCAAGCACCCGACATCAAGCCGAG	1474
OY	1261	GGCAGTCCCACCAAAGTGCAGAAAGAGTGCAGCTTCAACGACCGAACCCGCTTCCGGCCC	1320
Dd	1475	GGCAGTCCCACCAAAGTGCAGAAAGAGTGCAGCTTCAACGACCGAACCCGCTTCCGGCCC	1534
OY	1321	TGCGTGGGCTCCAAAAGTTCTCAGCCCAAAAACCAATGATAGATGCTGACACAGCCCTTGGC	1380
Dd	1535	TGCGTGGGCTCCAAAAGTTCTCAGCCCAAAAACCAATGATAGATGCTGACACAGCCCTTGGC	1599
OY	1381	ACTGATGATGTATATGATGAAAAAGATGCCAGTGTATGTTATCAATGATGAAGACTCTCAC	1440
Dd	1595	ACTGATGATGTATATGATGAAAAAGATGCCAGTGTATGTTATCAATGATGAAGACTCTCAC	1654
OY	1441	CCACCACTTAAACCTGTCAATTCGAGCTATCAGAAATTAATGAATTTCAATGTTGGCAAAACGG	1500
Dd	1655	CCACCACTTAAACCTGTCAATTCGAGCTATCAGAAATTAATGAATTTCAATGTTGGCAAAACGG	1714
OY	1501	AAGTTTAAAGAAAAGCTTAACGTCATATGATGATTAAGAAAGTGCATTGGAACAATATTCGCT	1560
Dd	1715	AAGTTTAAAGAAAAGCTTAACGTCATATGATGATTAAGAAAGTGCATTGGAACAATATTCGCT	1774
OY	1561	GGTCATCTGCAATGTTGTGTGAAATTAAGACCTTCAACACGCTGTTGATCAAAATTCCTT	1620

DB 1775 GGTGATCTGGACATGTTGTAGATTAAGCCCTTCAACAGCTGTGATCAAAATCTT 1834
1621 GGAAGAGGCAATCAATCAGATTAAGAGCCGAGAGAAATTAACAGACAGACATGAG 1680
1835 GGAAGAGGCAATCAATCAGATTAAGAGAGCCGAGAGAAATTAACAGACAGACATGAG 1894
1681 ACCACAGAGCATCTAGTATGCTCGGTGGGTGTCAAGGTTGAAAAACAGTACAGTCC 1740
1895 ACCACAGAGCATCTAGTATGCTCGGTGGGTGTCAAGGTTGAAAAACAGTACAGTCC 1954
1741 ATGAGATCCAGATGAGTGGCTGCTACAGATCTATCAACAGTCTCTTGAGAAAGCTCT 1800
1955 ATGAGATCCAGATGAGTGGCTGCTACAGATCTATCAACAGTCTCTTGAGAAAGCTCT 2014
1801 GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGATCT 1860
2015 GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGATCT 2074
1861 GACTATCAAGCCCTGTGATGATAGCAAGATCTTTGCGGTTCCGACAAAAACAGTGGCTGC 1920
2075 GACTATCAAGCCCTGTGATGATAGCAAGATCTTTGCGGTTCCGACAAAAACAGTGGCTGC 2134
1921 TTATCCAGATCAATCTAGTGCATCTGAGAGGCTGCAAGTCAATTCGACGCCAAT 1980
2135 TTATCCAGATCAATCTAGTGCATCTGAGAGGCTGCAAGTCAATTCGACGCCAAT 2194
1981 GAGTTCAGTCCGAGACTTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACAG 2040
2195 GAGTTCAGTCCGAGACTTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACAG 2254
2041 GTGCCAATTAATGATCAAGCCGATGCTGACAGTGGCCACCAACCATTTGCAACCA 2100
2255 GTGCCAATTAATGATCAAGCCGATGCTGACAGTGGCCACCAACCATTTGCAACCA 2314
2101 ATAAATACGGCAACCAAGCCAGGACGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2160
2315 ATAAATACGGCAACCAAGCCAGGACGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2374
2161 GCCATCAAGCATCTGCCAGGCGGAGGAGAACTCTGCAACCTTACAGGCTTACAGGAA 2220
2375 GCCATCAAGCATCTGCCAGGCGGAGGAGAACTCTGCAACCTTACAGGCTTACAGGAA 2434
2221 AGCATTTCTGAGCTCAACACCTGCTTTGTTGCTCCAGAGAAATGTTCAAGTTGCAAG 2280
2435 AGCATTTCTGAGCTCAACACCTGCTTTGTTGCTCCAGAGAAATGTTCAAGTTGCAAG 2494
2281 TCAAAATCTACCAAGGACGCTTCTATGAGGAAAGCTTTGACATGGAGAGAGAACTCTG 2340
2495 TCAAAATCTACCAAGGACGCTTCTATGAGGAAAGCTTTGACATGGAGAGAGAACTCTG 2554
2341 TTGTCTGTCTGTCCATGTGCGGAGGAACTTTGTTGTTGTTGTTGTTGTTGTTGTTG 2400
2555 TTGTCTGTCTGTCCATGTGCGGAGGAACTTTGTTGTTGTTGTTGTTGTTGTTGTTG 2614
2401 ATCAGGTGCAACGAGGAACTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGTCTCA 2460
2615 ATCAGGTGCAACGAGGAACTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGTCTCA 2674
2461 GAGAGCAAGATTTTACCCTCAATGAGGAGATCCAAATGTTTAACTGAAGAG 2520
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2521 GTGGGTCGCCAGAGAGACAGAGACAGACATTTTGTATGTCGCAACCGAGGCTGCCAGGAA 2580
2735 GTGGGTCGCCAGAGAGACAGAGACAGACATTTTGTATGTCGCAACCGAGGCTGCCAGGAA 2794
2581 GCTGCTTTGTCATCAAGCTCTTAAGAGCTGGAAGTCAAGATCATCTCAAGACATTTGT 2640
2795 GCTGCTTTGTCATCAAGCTCTTAAGAGCTGGAAGTCAAGATCATCTCAAGACATTTGT 2854
2641 AAGGAGAGAGAAATGATCAGATGCGCTCAGCTTGTCAATGTAATAA 2694

DB 2855 AAGCAGAGAGAAATGATCAGATGCTCCTCAGCTTGCCTCATGTCAAACTGAATATA 2908
RESULT 3
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: Lex-0160-USA
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
Query Match 97.4%; Score 2625.2; DB 4; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
DB 1 ATGAAGATGATGAGTCCGAGCGGAGGAGGAGGCTGTAATCTCGGACGCCGAGGAGC 60
106 ATGAAGATGATGAGTCCGAGCGGAGGAGGAGGAGGCTGTAATCTCGGACGCCGAGGAGC 165
61 GACGCGCTGCTACTGCTGAGGACCCGCGCGGACAGCTTGTGAGCGCGGAGGAGCCTG 120
166 GACGCGCTGCTACTGCTGAGGACCCGCGCGGACAGCTTGTGAGCGCGGAGGAGCCTG 225
121 AGGAGACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
226 AGGAGACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 285
181 TACAGAGTACGACAGGCTGCGGCGCAACGTCAGTACCGGCGGAGTCAAGTAACTACCTG 240
286 TACAGAGTACGACAGGCTGCGGCGCAACGTCAGTACCGGCGGAGTCAAGTAACTACCTG 345
241 TACAACTGTGAGAGACCCCGCGGCTGGGCGTTCACTACACGCTTTGTTTTCTC 300
346 TACAACTGTGAGAGACCCCGCGGCTGGGCGTTCACTACACGCTTTGTTTTCTC 405
301 CTGTGCTTGTGATGATGATTTTGTCAAGTCTTACATCCGAGACACAAATTTG 360
406 CTGTGCTTGTGATGATGATTTTGTCAAGTCTTACATCCGAGACACAAATTTG 465
361 GCCTCAAGTGGCTTGTATCTGAGGATTCGATGATGTTGTTGTTGTTGTTGTTGTTGTTG 420
466 GCCTCAAGTGGCTTGTATCTGAGGATTCGATGATGTTGTTGTTGTTGTTGTTGTTGTTG 525
421 ATCATTTGAATCTGTGCTGCGGTTGCTGTTGTGATATAGAGATGCAAGAAAGACTG 480
526 ATCATTTGAATCTGTGCTGCGGTTGCTGTTGTGATATAGAGATGCAAGAAAGACTG 540
481 AGCTTTGCTGAAACCCCTTCTGTGTTTATAGATACATGTTCTTATGCTTCAATPAGA 540
546 AGCTTTGCTGAAACCCCTTCTGTGTTTATAGATACATGTTCTTATGCTTCAATPAGA 645
541 GTTGTCTGCAAAATCTCAGGATATATTTTGTGCAAGTCTGCAAGTCTGCAAGTCTGCT 600
646 GTTGTCTGCAAAATCTCAGGATATATTTTGTGCAAGTCTGCAAGTCTGCAAGTCTGCT 705

QY	601	TTCTCAACAGATCTCTCCGATAGTGTGGCATATGACCCGAAAGGGAGAGCACTTGGAAATTACTG	660
Db	706	TTCTCAACAGATCTCTCCGATAGTGTGGCATATGACCCGAAAGGGAGAGCACTTGGAAATTACTG	765
QY	661	GGTTACAGTGTATTAAGTCTCAACAGAAAGAAATTAATCAGAGCTGGTACATAGATTTTGTG	720
Db	766	GGTTACAGTGTATTAAGTCTCAACAGAAAGAAATTAATCAGAGCTGGTACATAGATTTTGTG	825
QY	721	GTTCTTAATTTTTTGGTCTTTCTGTCTATCTGTGTGAAAAAGATGCCAATPAAAGATT	780
Db	826	GTTCTTAATTTTTTGGTCTTTCTGTCTATCTGTGTGAAAAAGATGCCAATPAAAGATT	885
QY	781	TCTACATATGCGAGATCTCTGTGTGGGGGCAATTAATCATTTGACAACTATTGGCTATGGA	840
Db	886	TCTACATATGCGAGATCTCTGTGTGGGGGCAATTAATCATTTGACAACTATTGGCTATGGA	945
QY	841	GACAAAACTCCCTACTTGGCTGGGAAAGATTCTTGTGCAAGCTTTGCACTCCCTGGC	900
Db	946	GACAAAACTCCCTACTTGGCTGGGAAAGATTCTTGTGCAAGCTTTGCACTCCCTGGC	1005
QY	901	ATTCTTTCTTTGCACTTCTGCGGGAATTTCTGGCTCAGGTTTTTGCAATTAAAGTACA	960
Db	1006	ATTCTTTCTTTGCACTTCTGCGGGAATTTCTGGCTCAGGTTTTTGCAATTAAAGTACA	1065
QY	961	GAACAAACCCGCAACAAACATTTGAGAAAAGAAAGAAACCAAGCTCCAACTCATTCAG	1020
Db	1066	GAACAAACCCGCAACAAACATTTGAGAAAAGAAAGAAACCAAGCTCCAACTCATTCAG	1125
QY	1021	TGTGTTGGCGTGAATGACGACGCTGATAGAAATCTGTTTCCATTGCAACCTGGAAAGCA	1080
Db	1126	TGTGTTGGCGTGAATGACGACGCTGATAGAAATCTGTTTCCATTGCAACCTGGAAAGCA	1185
QY	1081	CACTTGAAGGCGCTTGACACCTGCAAGCCCTACCAAGAAAGAAACAAAGGGAAGATCAAGC	1140
Db	1186	CACTTGAAGGCGCTTGACACCTGCAAGCCCTACCA-----	1220
QY	1141	AGTCGAAGCTPAAGTTTTAAGAGCGAGTGCATGAGTCCGAGGGGCAAGATAT	1200
Db	1221	--TCGAAGCTPAAGTTTTAAGAGCGAGTGCATGAGTCCGAGGGGCAAGATAT	1278
QY	1201	AAGAGCCGACAAAGCCTCAGTAGAGTATACAGAGAGTCCCAACGACCGAATCAACGCCGAG	1260
Db	1279	AAGAGCCGACAAAGCCTCAGTAGAGTATACAGAGAGTCCCAACGACCGAATCAACGCCGAG	1338
QY	1261	GGCAGTCCCAACCAAGGTCAAGAGAGCTGAGACTTCAACGACCGAACCCTCCGAGCC	1320
Db	1339	GGCAGTCCCAACCAAGGTCAAGAGAGCTGAGACTTCAACGACCGAACCCTCCGAGCC	1398
QY	1321	TGCTGCGCCTTCAAAAGTTCTCAGCCAAAACCAATGATAGATGCTGACACAGCCCTTGGC	1380
Db	1399	TGCTGCGCCTTCAAAAGTTCTCAGCCAAAACCAATGATAGATGCTGACACAGCCCTTGGC	1458
QY	1381	ACTGATGATATATGATGAAAAAAGAGAGCCAGTGTGATATGATCACTGGAAGACCTCAC	1440
Db	1459	ACTGATGATATATGATGAAAAAAGAGAGCCAGTGTGATATGATCACTGGAAGACCTCAC	1518
QY	1441	CCACCACCTTAAACCTGTCATTGAGCTATCAAGATTATGAATTATCATGTTGCCAAACGG	1500
Db	1519	CCACCACCTTAAACCTGTCATTGAGCTATCAAGATTATGAATTATCATGTTGCCAAACGG	1578
QY	1501	AAGTTTAAGGAAACGTTACGTCATATGATATGTTAAAGATGTTCATTGAAACATATTCTGCT	1560
Db	1579	AAGTTTAAGGAAACGTTACGTCATATGATATGTTAAAGATGTTCATTGAAACATATTCTGCT	1638
QY	1561	GGTCACTGAGACATGTGTGTGAAATTTAAAGCCTTCAACACAGCTTGATCAAAATTTCT	1620
Db	1639	GGTCACTGAGACATGTGTGTGAAATTTAAAGCCTTCAACACAGCTTGATCAAAATTTCT	1698
QY	1621	GGAAAGGGCAATACATCAGATTAAGAAAGCCGAGAGAAATTAACGACGAACATGAG	1680
Db	1699	GGAAAGGGCAATACATCAGATTAAGAAAGCCGAGAGAAATTAACGACGAACATGAG	1758

QY	1661	ACCAACAGACCACTCAGAGTACCTGGCTGGGTGCTCAAGGTGAAAACAGGTACAGTCC	1740
Db	1759	ACCAACAGACCACTCAGTATGCTGGTGGGTGCTCAAGGTGAAAACAGGTACAGTCC	1818
QY	1741	ATAGAGTCCAGAGCTGGACTGGCTCTAGACATCTATCAACAGAGTCTTCGGAAAGCTCT	1800
Db	1819	ATAGAGTCCAGAGCTGGACTGGCTCTAGACATCTATCAACAGAGTCTTCGGAAAGCTCT	1878
QY	1801	GCTTCAGCCTTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGACATCT	1860
Db	1879	GCTTCAGCCTTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGACATCT	1938
QY	1861	GACTATCAAAACCCGTCGAGATAGCAAAAGATCTTTGGAGTTCCGACAAAACAGTGGCTGC	1920
Db	1939	GACTATCAAAACCCGTCGAGATAGCAAAAGATCTTTGGAGTTCCGACAAAACAGTGGCTGC	1998
QY	1921	TTATTCAGATCACTAGTGGCCACATCTCGAGAGCCTGCAAGTTCAATCTGACGCCCAAT	1980
Db	1999	TTATTCAGATCACTAGTGGCCACATCTCGAGAGCCTGCAAGTTCAATCTGACGCCCAAT	2058
QY	1961	GAGTTCAAGTCCAGACATTTTCTACGGCTTAAGCCTTACTATGCAAGTCAAGCAACACAG	2040
Db	2059	GAGTTCAAGTCCAGACATTTTCTACGGCTTAAGCCTTACTATGCAAGTCAAGCAACACAG	2118
QY	2041	GTGCAATTTAGTCAAAAGGATGGCTCGACAGTGGCAGCCACCAACATTTGCAACCA	2100
Db	2119	GTGCAATTTAGTCAAAAGGATGGCTCGACAGTGGCAGCCACCAACATTTGCAACCA	2178
QY	2101	ATTAATACGGACCCCAAGCCAGCAGCACCACCACTTACAGATCCCACTCTCTCCCA	2160
Db	2179	ATTAATACGGACCCCAAGCCAGCAGCACCACCACTTACAGATCCCACTCTCTCCCA	2238
QY	2161	GCCATCAAGCATCTGGCCAGGCCAGAACTCTGCAACCTTAACCTTGAAGGCTTACAGAA	2220
Db	2239	GCCATCAAGCATCTGGCCAGGCCAGAACTCTGCAACCTTGAAGGCTTACAGAA	2298
QY	2221	AGCATTTCTGACGTCAACCACTGGCTTTGTCCTCCAAAGGAAATGTTCAAGTGTGCACAG	2280
Db	2299	AGCATTTCTGACGTCAACCACTGGCTTTGTCCTCCAAAGGAAATGTTCAAGTGTGCACAG	2358
QY	2281	TCAAATCTCACCAAGAGCCGTTCTATAGAGAAAGCTTTGACATGGAGAGAAACTCTG	2340
Db	2359	TCAAATCTCACCAAGAGCCGTTCTATAGAGAAAGCTTTGACATGGAGAGAAACTCTG	2418
QY	2341	TTTGCTGCTGCTGCCATAGTGGCCGAAGAAGCTTGGGCAAACTTTTGCTGTCGCAAAACTG	2400
Db	2419	TTTGCTGCTGCTGCCATAGTGGCCGAAGAAGCTTGGGCAAACTTTTGCTGTCGCAAAACTG	2478
QY	2401	ATCAGAGTGCACCGAGAACTGAATATCAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA	2460
Db	2479	ATCAGAGTGCACCGAGAACTGAATATCAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA	2538
QY	2461	GGCAGCCCAAGATTTTAAACCCCAAAATGAGAGGAATCCAAATTTGTTATPACTGATGAAGAG	2520
Db	2539	GGCAGCCCAAGATTTTAAACCCCAAAATGAGAGGAATCCAAATTTGTTATPACTGATGAAGAG	2598
QY	2521	GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGAATGCGCAGCCGACGAGCCTGCAGGGAA	2580
Db	2599	GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGAATGCGCAGCCGACGAGCCTGCAGGGAA	2658
QY	2581	GCTGCTTTTGATCAGACTCTCTTAAGACCTGGAAGTCAAGATCATCTCAGAGCATTTGT	2640
Db	2659	GCTGCTTTTGATCAGACTCTCTTAAGACCTGGAAGTCAAGATCATCTCAGAGCATTTGT	2718
QY	2641	AAAGCAGAGAAAGTACAGATGCCCCCTCAGCTTGCTCTATGTCAAACTGAAATTA	2694
Db	2719	AAAGCAGAGAAAGTACAGATGCCCCCTCAGCTTGCTCTATGTCAAACTGAAATTA	2772

RESULT 4
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736

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; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiehe, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. 676736e1 Human Ion Channel Protein and
; FILE REFERENCE: Lex-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-3

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Query Match      97.4%; Score 2625.2; DB 4; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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QY 1 ATGAAGATGTGGAGTCGGGCGGAGGAGGAGTCTGTAACCTCGGACCGGACGAGGAGC 60
DB 165 ATGAAGATGTGGAGTCGGGCGGAGGAGGAGTCTGTAACCTCGGACCGGACGAGGAGC 224
QY 61 GACGGCTCTCTACTGCTGGGACCCCGCGCCACGCTTGATGGGCGGAGGAGGAGCCTG 120
DB 225 GACGGCTCTCTACTGCTGGGACCCCGCGCCACGCTTGATGGGCGGAGGAGGAGCCTG 284
QY 121 AGGAGAGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 285 AGGAGAGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 344
QY 181 TACACAGATAGCAGAGTCCGCGGCGCAACGTCATGATCCGGGAGGAGGAGGAGGAGG 240
DB 345 TACACAGATAGCAGAGTCCGCGGCGCAACGTCATGATCCGGGAGGAGGAGGAGGAGG 404
QY 241 TACAAAGTCTGAGAGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 405 TACAAAGTCTGAGAGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 464
QY 301 CTGTGCTTGGTGTGATTTTGTGATGTTTCTACATCCCTGAGACACAAATTTG 360
DB 465 CTGTGCTTGGTGTGATTTTGTGATGTTTCTACATCCCTGAGACACAAATTTG 524
QY 361 GCCTCAAGTTCCTTGAATCCGAGATTCGATGATTCGATTCGATTCGATTCGATTCG 420
DB 525 GCCTCAAGTTCCTTGAATCCGAGATTCGATGATTCGATTCGATTCGATTCGATTCG 584
QY 421 ATCATTCGAATCTGATCGGAGTTCGATTCGATTCGATTCGATTCGATTCGATTCG 480
DB 585 ATCATTCGAATCTGATCGGAGTTCGATTCGATTCGATTCGATTCGATTCGATTCG 644
QY 481 AGGTTTGTCTGAAAGCCCTTCTGTATAGATACCATTTCTTATCGCTTCAATAGCA 540
DB 645 AGGTTTGTCTGAAAGCCCTTCTGTATAGATACCATTTCTTATCGCTTCAATAGCA 704
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DB 705 GTTGTCTTCTGCAAAAACCTCAGGGTAATATTTTTCACAGTCTGACCTGAGAGTCTCG 764
QY 601 TTCTCTACAGATCTCTCGCATGTGTGCGCATGACCGAAGGAGGAGGAGGAGGAGGAG 660
DB 765 TTCTCTACAGATCTCTCGCATGTGTGCGCATGACCGAAGGAGGAGGAGGAGGAGGAG 824
QY 661 GGTTCAAGTGTATATCTCAACAGGAATTAATCAAGCTTGTGATTAAGATTTTGTG 720

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DB 825 GGTTCAAGTGTATATCTCAACAGGAATTAATCAAGCTTGTGATTAAGATTTTGTG 884
QY 721 GTTCTTATTTTTCGTCCTTTCCTGTCATCTGTGAGAAAGAGATCCAAATTAAGATT 780
DB 885 GTTCTTATTTTTCGTCCTTTCCTGTCATCTGTGAGAAAGAGATCCAAATTAAGATT 944
QY 781 TCTACATATGAGATGCTCTGTGTGGGCACAATTAATTAAGATTAAGATTAAGATTA 840
DB 945 TCTACATATGAGATGCTCTGTGTGGGCACAATTAATTAAGATTAAGATTAAGATTA 1004
QY 841 GACAAACCTCCCTTAACCTGCTGGGAGATTTGTTTCTGACAGGCTTGTGACCTCTG 900
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QY 901 ATTCTTCTTCTGACCTTCTGCGGCAATCTTGCTCAGGTTTGTGATTAAGATTAAG 960
DB 1065 ATTCTTCTTCTGACCTTCTGCGGCAATCTTGCTCAGGTTTGTGATTAAGATTAAG 1124
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DB 1280 --TCAGAAAGCTTAAGTTTAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1337
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DB 1338 AAAGGCGGAAACCCGCGAGTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1397
QY 1261 GGCAGTCCCAAGAGTCCAGAAAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
DB 1398 GGCAGTCCCAAGAGTCCAGAAAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1457
QY 1321 TCGCTGCGCTCTGAAAAGTTCTGACGCAAAACGATGATGATGCTGACACAGCCTT 1380
DB 1458 TCGCTGCGCTCTGAAAAGTTCTGACGCAAAACGATGATGATGCTGACACAGCCTT 1517
QY 1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1518 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1577
QY 1441 CCACCACTTAAACCTGTCATTCGAGCTATCAGAAATTAATTAATTAATTAATTAATTA 1500
DB 1578 CCACCACTTAAACCTGTCATTCGAGCTATCAGAAATTAATTAATTAATTAATTAATTA 1637
QY 1501 AAGTTTAAGAAAGTTCATTCGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1638 AAGTTTAAGAAAGTTCATTCGATGATGATGATGATGATGATGATGATGATGATGAT 1697
QY 1561 GGTCACTGGAACATGTTGTGATGATTAAGAAAGCTTCAAAACGATGATGATGATGAT 1620
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DB 1878 ATAGAGTCAAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1937

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QY 1801 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCACCTTTTGATGTGAACAGACATCT 1860
DB 1938 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCACCTTTTGATGTGAACAGACATCT 1997
QY 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGACAAAAAGTGGCTGC 1920
DB 1998 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGACAAAAAGTGGCTGC 2057
QY 1921 TTATCCAGATCACTAGTGGCAATCTCGAAGGCTGTGAAGTTCAATTCAGAGCCAAAT 1980
DB 2058 TTATCCAGATCACTAGTGGCAATCTCGAAGGCTGTGAAGTTCAATTCAGAGCCAAAT 2117
QY 1981 GAGTTAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2040
DB 2118 GAGTTAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2177
QY 2041 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAGCCCAACCAACCATTTGCAACCA 2100
DB 2178 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAGCCCAACCAACCATTTGCAACCA 2237
QY 2101 ATTAATACGGACCCCAAGCCGACCCCAACCACTTTAAGATCCCACTCTCTCCCA 2160
DB 2238 ATTAATACGGACCCCAAGCCGACCCCAACCACTTTAAGATCCCACTCTCTCCCA 2297
QY 2161 GCCATCAAGCATGCGCCAGGCGCAAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA 2220
DB 2298 GCCATCAAGCATGCGCCAGGCGCAAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA 2357
QY 2221 AGCATTTCTGACGTCAACACCTGCTTGTGCTCCAGAGAAATGTTCAAGTTGACAG 2280
DB 2358 AGCATTTCTGACGTCAACACCTGCTTGTGCTCCAGAGAAATGTTCAAGTTGACAG 2417
QY 2281 TCAAATCTCAAGGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAACTCTG 2340
DB 2418 TCAAATCTCAAGGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAACTCTG 2477
QY 2341 TTGTCGTCTGTCGCCATGCGGCGAAGGACTTGGGCAAACTTTGTCGTGCAAACTCG 2400
DB 2478 TTGTCGTCTGTCGCCATGCGGCGAAGGACTTGGGCAAACTTTGTCGTGCAAACTCG 2537
QY 2401 ATCAGGTGCAACGAGAACTGAATATCAACTTTCAGGAGTGAAGTCAAGTGGCTCAG 2460
DB 2538 ATCAGGTGCAACGAGAACTGAATATCAACTTTCAGGAGTGAAGTCAAGTGGCTCAG 2597
QY 2461 GGCAGCCAGATTTTAACTCCCAATGAGGGAATCCAAATTTGTTAATGATGAAG 2520
DB 2598 GGCAGCCAGATTTTAACTCCCAATGAGGGAATCCAAATTTGTTAATGATGAAG 2657
QY 2521 GTGGGTCCGAAAGACAGAGACAGACACTTTTGAATGCGGCAAGGAGCTGCAAGGAA 2580
DB 2658 GTGGGTCCGAAAGACAGAGACAGACACTTTTGAATGCGGCAAGGAGCTGCAAGGAA 2717
QY 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGAAGGTCAGATCATCTCAGACATTTGT 2640
DB 2718 GCTGCTTTGATCAGACTCTCTAAGGACTGAAGGTCAGATCATCTCAGACATTTGT 2777
QY 2641 AAGCAGAGAGAAAGTACAGATGCTTCAAGCTTCAATGCTCAAACTGAATAA 2694
DB 2778 AAGCAGAGAGAAAGTACAGATGCTTCAAGCTTCAATGCTCAAACTGAATAA 2831

RESULT 5
US-09-949-016-1823
; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

QY 1801 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCACCTTTTGATGTGAACAGACATCT 1860
DB 1938 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCACCTTTTGATGTGAACAGACATCT 1997
QY 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGACAAAAAGTGGCTGC 1920
DB 1998 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGACAAAAAGTGGCTGC 2057
QY 1921 TTATCCAGATCACTAGTGGCAATCTCGAAGGCTGTGAAGTTCAATTCAGAGCCAAAT 1980
DB 2058 TTATCCAGATCACTAGTGGCAATCTCGAAGGCTGTGAAGTTCAATTCAGAGCCAAAT 2117
QY 1981 GAGTTAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2040
DB 2118 GAGTTAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2177
QY 2041 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAGCCCAACCAACCATTTGCAACCA 2100
DB 2178 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAGCCCAACCAACCATTTGCAACCA 2237
QY 2101 ATTAATACGGACCCCAAGCCGACCCCAACCACTTTAAGATCCCACTCTCTCCCA 2160
DB 2238 ATTAATACGGACCCCAAGCCGACCCCAACCACTTTAAGATCCCACTCTCTCCCA 2297
QY 2161 GCCATCAAGCATGCGCCAGGCGCAAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA 2220
DB 2298 GCCATCAAGCATGCGCCAGGCGCAAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA 2357
QY 2221 AGCATTTCTGACGTCAACACCTGCTTGTGCTCCAGAGAAATGTTCAAGTTGACAG 2280
DB 2358 AGCATTTCTGACGTCAACACCTGCTTGTGCTCCAGAGAAATGTTCAAGTTGACAG 2417
QY 2281 TCAAATCTCAAGGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAACTCTG 2340
DB 2418 TCAAATCTCAAGGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAACTCTG 2477
QY 2341 TTGTCGTCTGTCGCCATGCGGCGAAGGACTTGGGCAAACTTTGTCGTGCAAACTCG 2400
DB 2478 TTGTCGTCTGTCGCCATGCGGCGAAGGACTTGGGCAAACTTTGTCGTGCAAACTCG 2537
QY 2401 ATCAGGTGCAACGAGAACTGAATATCAACTTTCAGGAGTGAAGTCAAGTGGCTCAG 2460
DB 2538 ATCAGGTGCAACGAGAACTGAATATCAACTTTCAGGAGTGAAGTCAAGTGGCTCAG 2597
QY 2461 GGCAGCCAGATTTTAACTCCCAATGAGGGAATCCAAATTTGTTAATGATGAAG 2520
DB 2598 GGCAGCCAGATTTTAACTCCCAATGAGGGAATCCAAATTTGTTAATGATGAAG 2657
QY 2521 GTGGGTCCGAAAGACAGAGACAGACACTTTTGAATGCGGCAAGGAGCTGCAAGGAA 2580
DB 2658 GTGGGTCCGAAAGACAGAGACAGACACTTTTGAATGCGGCAAGGAGCTGCAAGGAA 2717
QY 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGAAGGTCAGATCATCTCAGACATTTGT 2640
DB 2718 GCTGCTTTGATCAGACTCTCTAAGGACTGAAGGTCAGATCATCTCAGACATTTGT 2777
QY 2641 AAGCAGAGAGAAAGTACAGATGCTTCAAGCTTCAATGCTCAAACTGAATAA 2694
DB 2778 AAGCAGAGAGAAAGTACAGATGCTTCAAGCTTCAATGCTCAAACTGAATAA 2831

Query Match 19.2%; Score 518.4; DB 4; Length 2196;
Best Local Similarity 60.1%; Pred. No. 1.2e-143;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;
PRIORITY APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1823

QY 217 TACCGCGGCTGACAGAACTGATCAACAGTGTGAGAGACCCCGCGGCTGGCTTC 276
DB 181 TACCGCGGCTGACAGAACTGAGGAGTACAGCTGTGAGAGCGGCCCGCGGCTGGCTTC 240
QY 277 ATCTACAGCGCTTGTGTTTCTCTCTGTCTTGTGTTGTTGATTTGCTGATTTTCT 336
DB 241 GTCTACAGCTCTCATATTTTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 337 ACCATTCCTGACACACAAATTTGGCTCAAGTTGCTTGTATCTGAGATTCGTGATG 396
DB 301 ACTATTCAGAGACACACAACTTGCACAGAGTCTCTCATCTTGAATTCGTGATG 360
QY 397 ATTGCTGCTTTGTTGTTGATTCATTCATTCGATCTGCTGCGGCTGCTGCTGCTGCTG 456
DB 361 ATCTGCTTTGCTGCTGTTGAGTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 457 TATAGAGATGCAAGAAAGTGAAGTGTGCTGCAAAAGCCCTTCTGTATTAATATAC 516
DB 421 TACCGAGATGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 517 ATTGTTCTTATGCTTCAATATGATGTTGTTGCAAAAACTCAGAGTAAATTTTGGC 576
DB 481 ATCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 577 ACCTGTCACATCAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636
DB 541 ACCTGTCACATCAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 637 AAGGAGAGCACTTGAATTAATCTGAGTTCAGTGTGTTATGCTCAGACAGAAATTAATC 696
DB 601 CGCGGCGCACCTGGAAGCTGCTGCGGCTCAGTGTCTAGCGCATAGCAAGAGCTGATC 660
QY 697 ACAGCTTGTATATAGATATTTTGTGTTTGTATTTTGTGTTTGTGTTTGTGTTTGTG 756
DB 661 ACCGCTGCTATCAGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 757 GAAAGAGATGCAATTAAGATTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCT 816
DB 721 GAAAGAGATGCAATTAAGATTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCT 780
QY 817 ACATTCAGCAATTCAGGCTATGAGTGAACAACTCCCTTAATCTGCTGAGGAATGCTT 876
DB 781 ACATTCAGCAATTCAGGCTATGAGTGAACAACTCCCTTAATCTGCTGAGGAGCTG 840
QY 877 TCTGCAAGCTTTGCACTCTTGGCATTTTCTTCTTGTGCACTTCTGCGGCAATTTCT 936
DB 841 GCTGCTGCTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 937 TCAGGTTTGTATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 996
DB 901 TCCGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 997 AACCCAGCTCCCACTATTCAGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
DB 961 ATCCCGGAGCAACCTATTCAGGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020

QY 1057 GTTTCATTGCAACCTGGAAGCCACCTTGAAAGCCTTGCAACCTGACG----- 1107
Db 1021 GCCTACCTGACAGCCACCTGTGACTACTATGACATATCCTCCATCTTTCAGAGAGCTG 1080
QY 1108 CCTACCAAGAAAGAAAGAGGGAAGCATCAGACATGCAAGAGTA----- 1152
Db 1081 GCCCTCTTGTGGAGACGTGCAACGGGCCCGCAATGGGGGCTTACGGCCCTGAGAGTG 1140
QY 1153 ----- 1152
Db 1141 CGGCGGGGCGCGGTACCCGACGAGCACTCCCGTTACCCCGCGCTTGACCTCCAC 1200
QY 1153 -----AGTTTAAAGACGA 1167
Db 1201 CGGCGGGGAGACCTCTTCTGCGCTGGGAAAGACGCGGATGGGATCAAAAGACGCG 1260
QY 1168 GTGCGCATGGCTAGCCCGGAGGCGCA-----GTAATTAAGCGGACAAAGCTTAGTA 1221
Db 1261 ATCCCGATGGGAGCTCCAGCGCGGAGCGGATCTTCCAGAGCATCTGGACCTCCA 1320
QY 1222 GGTGACAGAGGTCCCGCAAGACCGACATCAGACCGGAG---GCATGCCACCAAGTG 1278
Db 1321 ACATATGCCACCTCCCGAAGACCGAGCGAGTGGGAGCCACCGCCCAAGAGTG 1380
QY 1279 CAGAAAGCTGAGCTTCAACGACCGAACCCGCTTCGCGCTCGCTGCGCTCAAAAGT 1338
Db 1381 CAAGAAGCTGGAGCTTCAATGACCGACCCGCTTCGCGGATCTGAGAGCTC----- 1434
QY 1339 TCTCAGCCAAAACCAAGTATAGTGTGACACAGCCCTTGAGCATGATATATATAT 1398
Db 1435 -----AAACCCGACCTCTGTGAGATGCC---CCTCAGAGAAATGACAGAG 1482
QY 1399 GAAAAAGATGCCAGTGTATGTATGATGAGAAAGACCTGACCCGACCACTTAAACTGTC 1458
Db 1483 GAGAAAGCTACCAAGTGTAGCTCAGCGTGGAGACATATGCTGCTGTAAGACAGTC 1542
QY 1459 ATTGAGCTATCAAAATTAATTAATTTCAATGTTGCAAAACGAAAGTTTAAAGAAAGTTA 1518
Db 1543 ATCCGCTCATCGAGATCTCAAGATTCCTGTGGCCAAAGAAATTAAGAGACAGTCG 1602
QY 1519 CTTCCATATGATGATTAAGAAATGATGATTAATTAATTTCTGCTGTGATCTGACATGTTG 1578
Db 1603 CAGCCGTACGAGGTGAAGACGTCAATTAAGCATCAAGGCCCACTGAGCAATGCTG 1662
QY 1579 TGTAGATTAATTAAGCCTTCAAAACGTTGTGATCAAACTCTTGAAAGAGGCG---AAATC 1635
Db 1663 GGGCGGATCAAGAGCTTGCAAACTCGGGTGGACCAATTTGTGGGTGGGGGCGCGGAGC 1722
QY 1636 ACATCAGATTAAGAGAGCGGAGAAATTAACAGCAAGCATGAGCAACAGATCTTC 1695
Db 1723 AGGAAGGCGCGGAGAGAGGCGGCAAGGGGCGCTCCGAGCGGAGGTGGATGAATATC 1782
QY 1696 AGTATGCTGGGTGGGTGCTCAAGGTTGAAAGAAAGAGTACAGTCCATTAAGTCAAGCTG 1755
Db 1783 ACATGATGAGAGCGCGTGTCAAGGTGGAAGAGAGTCAAGTCCATCAAGACAAAGCTG 1842
QY 1756 GACTGCTACTAGACATCTATCAACAGTCTTCCGAAAGGCGTGGCCCTCAGCCCTCGT 1815
Db 1843 GACCTGCTTGTGGCTTCTATTCGCGCTGCTGCG-----GCTTGGGACCTTGCGGACG 1896
QY 1816 TTGGCTTCAATTCAGATCCCACTTTTGAATGTAAGACATCTGACTATCAAGAGCTT 1875
Db 1897 CTGGGCGCGGTGCAAGTGGCGGTGTCGACCCGACATCACTCGAGCTACACAGCCCT 1956
QY 1876 GTGATAGCAAAAGATTTTGGGCTTCCGACAAA 1909
Db 1957 GTGACCAAGAGACATCTCGTCTCCGACAGA 1990

RESULT 6
US-09-492-361-1
Sequence 1, Application US/09492361

Patent No. 6794161
GENERAL INFORMATION:
APPLICANT: JENTSCH, Thomas J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
FILE REFERENCE: 2815-127P
CURRENT APPLICATION NUMBER: US/09/492,361
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 2335
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2335)
NAME/KEY: CDS
LOCATION: (83)..(2170)
US-09-492-361-1

Query Match 19.2% Score 518.4; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 1.3e-143;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

QY 217 TACCGCGGAGTGCAGAACTACCTGTACAAAGTGTGAGAGACCCGCGGCTGGCGCTTC 276
Db 320 TACCGCGGCTGCAGAACTGGGCTACAAAGTGTGAGAGCGGCGCGGCTGGCGCTTC 379
QY 277 ATCTACACGCTTGTGTTTCTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 336
Db 380 GTCTACACGCTTCTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 439
QY 337 ACCATCCCTGAGACACAAATGCGCTCAAGTTGCTCTTATCTGAGATCTGAGATCTGATG 396
Db 440 ACTATCCAGAGACACAGAACTTGCACAAAGTGTCTCTCATTTTGAATTCGATG 499
QY 397 ATTGCTCTTGTGTTGTTGAGTTCAATGAAATCTGCTGCGGTTGCTGTTGTTGTTGTTG 456
Db 500 ATCGGTTTCTGCTGTTGAGTATGATGTCGGGCTGTGTCGCGGATGCTGCGCGC 559
QY 457 TATGAGATGCAAGAGACCTAGGTTGCTGAAAGCCCTTCTGTGTTATGATAC 516
Db 560 TACCAGAGATGCAAGGTCGCTTCGCTTGCAGAAAGCCCTTCTGTGATCACTGCTTC 619
QY 517 ATTGTTCTTATCGCTTCAATGAGATGTTTCTGCAAAACCAAGGTAATTTTTC 576
Db 620 ATCGTTCTGCTGCTCGGTGCGGTCAATCGCCGCGGTACCAAGGCAATCTTCCGC 679
QY 577 ACGTCTGACTCAGAAAGTCTCGTTTCTCAAGATCTCCGATGTCGATGAGACGA 636
Db 680 ACGTCCGCGTCCGAGATCGCTCTCTGCAATCTCGGCAATGTCGATGAGACGCG 739
QY 637 AGGGAGGCACTTGAATTAACGAGTTCAAGTGTATGCTACAGCAAGAAATTAATC 696
Db 740 CGCGCGGACACTGGAAGCTCTGGGCTCAAGTGTCTACGCGCATAGCAAGAGCTGATC 799
QY 697 ACAGCTGTGATATAGATTTTGTGTTTATTTTGTCTTCTGCTGATCTGATG 756
Db 800 ACCGCTGTGATATCGGTTCTGCTGATCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 859
QY 757 GAAAAAGATGCAATTAAGATTTTCAATATGAGATGCTCTGTTGGGCGCAATTT 816
Db 860 GAGAAAGACGCACTCCGACTTCTCTCTACGCGCATGCTGCTGTGGGAGAGATTT 919
QY 817 ACATTGACATATTGCTATGAGAGCAAACTCCCTTAATCTGGCTGGGAAGATTGCTT 876
Db 920 ACATTGACAAACATCGCTATGAGAGCAACGCGCACATAGCTGGGAGAGGTTCTCTG 979
QY 877 TCTGAGGCTTGAATCTCTGAGATTTCTTCTTGTGACTTCTGCGCGGCAATCTTGGC 936
Db 980 GCTGCTGCTTGGCTTATCTGGGATCTCTTCTTGTGCTGCTGCGGCAATCTTGAAC 1039

937 TCAGGTTTGCAATTAAAGTACAAAGAACAAACCCGCAAGAAACCTTTGAGAAAAGAGG 996
1040 TCCGGCTTTGCCCTGAAAGGTCACAGAGACGACCCGAGAAAGCACTTCGAGAAAGGAGG 1099
997 AACCCAGCTGCCAACTTCATTCAGTGTGTTGGCGTAGTTACGAGCTGATGAGAAATCT 1056
1100 ATGCGGAGAGCAACCTCATTCAGAGCTGCGCTGGCTGTATCTCAACGATATGAGCCGG 1159
1057 GTTTCATTTGCAACCTGGAAGCCACACTTGAAGCCCTTGACACCTGACG----- 1107
1160 GCGTACCTGACAGCACCTGTACTATGACAGTATCTCCCTCCATCTTCAAGAGACTG 1219
1108 CTTACCAAGAAAGAACAGGGGAGATCAATCAAGCTGAGAGCTA----- 1152
1220 GCCTCTTGTGTTAGACAGTGCACAGGCGCGGCAATGGGGGCTTACGCGCCCTGAGAGTG 1279
1153 ----- 1152
1280 CGGCGGGGCGCGGTACCGGACGAGCACCTCCGTTACCCGCGCTTGCCACCTGCGAC 1339
1153 -----AGTTTAAAGAGCGA 1167
1340 CGGCGGGGCGGACCTTCCTTCTGCGCTGGGAAAAGACGCGGATGGGCATCAAGACCGC 1399
1168 GTGCGCATGCTAGCCCGGAGGCGCAGAG-----GTATTAAGAGCCGACAAAGCCTCAGTA 1221
1400 ATCCGCTATGGGCACTCTCCAGCGCGGAGCGGGTCTTTCAGAGACAGCTGGACCTCCA 1459
1222 GGTGACAGAGGTGTCACCAAGCACCGACATGACAGCCGAGG---GCAGTCCACCAAGAGT 1278
1460 ACAATGCCACCTCCCAAGCAGAGCAGGTGGTGAAGGCAACAGCCCAACCAAGGTG 1519
1279 CAGAAAGCTGAGAGCTTCAACGACCGAACCCGCTTCCGCGCTGCTGCGCTTCAAAAGT 1338
1520 CAAAGAGCTGAGCTTCAATGACCGGACCGGCTTCCGGGCACTCTGAGACTC----- 1573
1339 TCTCAGCAAAACCAAGTATGATGATGACACAGCCCTTGCACTGATGATATGAT 1398
1574 -----AAACCCGCACTCTGCTGAGAGATGCC---CTTCAGAGAAAGTAGCAGAG 1621
1399 GAAAGAGATGCGAGTGTGATGATGATCAGTGAAGACCTCAACCCGACCACTTAAACCTGTC 1458
1622 GAGAAAGCTACCAAGTGTGAGCTCAAGGTGACGACATCAATGCTGTGAGAGAGCTC 1681
1459 ATTGAGACTATCAGATTAATGAATTTGATGTTGCAAAAGGAAAGTTTAAAGAAAGTTA 1518
1682 ATCCGCTCCATCAGAGATTCTCAAGTTCCTGTGGCCAAAGAAATTCAGAGAGACACTG 1741
1519 GGTCAATATGATGTAAAGATGTCATGAACAATATTTCTGCTGATCCTGAGCATGTTG 1578
1742 CGACCGTAGCACTGAAGAGAGCTGATTTGAGAGTACTCAGAGAGCCACCTGAGCATGCTG 1801
1579 TGTGAATTTAAAGCCTTCAAGACAGTGTGATCAAAATTTCTTGAAAAGGGC---AAATC 1635
1802 GCGCGGATCAAGAGCCTGCAAACTCGGGGTGACCAAAATTTGGGTGGGGGCGCGGGGAGC 1861
1636 ACATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAGAAATGAGACACAGAGATCTC 1695
1862 AGGAAGGCCGAGGAGAGAGGCGACAAAGGGCCCTCCGACCGGAGGTGTGATGAATTC 1921
1696 AGTATGCTCGGTGGGGGTGCAAGGTTGAAGAAAAGGTAAGTCAATAGAGTCCAAAGCTG 1755
1922 AGCATATGAGAGCGGTGTCAGAGGTGAGAGAGAGGTGCAATGCTCATGAGCACAAGCTG 1981
1756 GACTGCTACTAGACATCTATCAACAGAGTCTTGGAAAGGCTGTGCTGAGCCCTGCGCT 1815
1982 GACTGCTGTGGGCTTCTATTCGCGCTGCTG-----GCTCTGACACTCGGCGAGC 2035
1816 TTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGACATGTGACTATCAAGCCCT 1875
2036 CTGGGCGCGCTGAAAGTGGCGGTGTCGACCCGACATCACTTCGACACAGGCCCT 2095
1876 GTGATATGCAAAAGATCTTTCGGGTTCCGACAAA 1909

Db 2096 GTGAGACCAGAGACATCTCCGTCCGACAGCA 2129
RESULT 7
US-09-177-650-88
; Sequence 88, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2271)
US-09-177-650-88
Query Match 19.2%; Score 516; DB 3; Length 2273;
Best Local Similarity 57.6%; Pred. No. 6,4e-143;
Matches 1030; Conservative 2; Mismatches 684; Indels 72; Gaps 4;
64 GCGCTCTACTGCTGAGGACCCGCGGCGCACGCTTGAGGCGGCGGTGAGGCTGAGG 123
67 GCGCTGTGGGCTGAGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 126
124 GAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 183
127 GCGGCGCTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
184 ACAGTAGGACAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 243
187 GGAAGCGGAGAGCGCCGCAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
244 AACGTGCTGAGAGAGACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 303
247 AACGTGCTGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306
304 GTCTTGTGCTGATGATTTGTGATGATTTGTGATGATTTGTGATGATTTGTGATGAT 363
307 GTTCTCTGCTGCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 366
364 TCAAGTGTGCTGATGATTTGTGATGATTTGTGATGATTTGTGATGATTTGTGATGAT 423
367 GAGGGGCGCTTCAACATCTTGAAGATGATGATGATGATGATGATGATGATGATGAT 426
424 ATTGCAATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 483
427 GTGAGATATCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 486
484 TTGCTGGAAGCGCTTCTGCTGATTAATGATTAATGATTAATGATTAATGATTAATGAT 543
487 TTGCGCAGGAACCGCTTCTGCTGATTAATGATTAATGATTAATGATTAATGATTAATG 546
544 GTTTCGCAAAACCTCAGGGAATAATTTTGGCAGGCTGCACTCAGAAAGTCCGTTTC 603
547 CTGGCTGCTGTTCCAGGGCAATGCTTGGCAATGCTGCGGCTTGGAGCTTGGGCTTC 606
604 CTACAGATCTCCGACAGTGTGCGACGACCAAGGGGAGGCACTTGAATTAATGAGGT 663

Db 607 TTGCAAACTCTTGCGATGATCCGTATGACCGGAGGGGTGCGACCTTGAGACTCTTGGGA 666
Qy 664 TCAGTGTCTTTATGCTCAGACGAAGAATTATCAGAGCTTGTGATCATAGATTTTGGTT 723
Db 667 TCGGTAGTCTAGCTCAGACGAAGAGCTGTGATCTGCTGTGATCACTTGGCTTCTCTG 726
Qy 724 CTATATTTTTCGTCTTCTCTTCTCTATCTGTGTGAAAAGAGATGCCAATAAAGATTTTCT 783
Db 727 CTCATCTGAGCCCATTTCTGGGTGATCTTGGCAGAAAAGGTGAGATGACCATTTGAC 786
Qy 784 ACATATGAGATGCTCTGTGTGGGGCACAATTACATTTGACAACTTTGGATATGGAGAC 843
Db 787 ACCTAGCAGATGATCTGTGTGGGTCTGATCACCCTGACGACATGTGCTACGGGAGC 846
Qy 844 AAAAATCCCCCTAATTTGGCTGGAGATGCTTTCTGACAGGCTTTGCACTCTTGGCATTT 903
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Qy 904 TCTTTCTTTGCACTTCTGCGGGCATTTCTGTGCTCAGGTTTTCATTTAAAGTACAGAA 963
Db 907 TCGTTCTTTGCTCTTCCGGCTGGCATTTTGGGATCCGGCTTGGCCCTGAAGTCCAAAG 966
Qy 964 CAACACCGCAGAAAACATTTGAGAAAAGAGAACCCGCTGCCAAGCTCATTTGACGT 1023
Db 967 CAGCATCGGAAAAACATTTGAGAAACGCGGAACTTGTGCGAGTCTGATCCAGTCT 1026
Qy 1024 GTTTGGCTGATGTTACCGAGCTGAT----- 1047
Db 1027 GCTGTGAGATTCTATCTACTAACCCTGACGCAACCGACCTGACCTCAAGTGGAGTAC 1086
Qy 1048 ---GAGAAATCTGTTTCCATTTGCACTTGAAGCCCATTTGAAGGCTTGTGACACTTGC 1104
Db 1087 TAGAGACGAAACATCTGTCTCCCATGTACAGCTCAAACTCAAACTATGGGGCTTCC 1146
Qy 1105 AG-----CCCTACCAAGAAAAGCAAGGGGAGCATCAAGCATGCAAGGCTAAGTTTA 1159
Db 1147 AGACTATCTCCACTCTTGAACCACTGAGCTGTGAGAAATCTCAAGCAAAATTTGGA 1206
Qy 1160 AAGAGGAGTGTGCGATGAGTACGCCCAAGGGGCGCAGATTTAAAGCCCAAGACCTTCA 1219
Db 1207 CTCACCTTCAGGAAAGAGCCACAGAGCCATCAACAAAGCCCGGAGGATGGCTGCC 1266
Qy 1220 TAGGTACAGAGAGTCCCAAGCATCAGATCAGAC----- 1256
Db 1267 AAGGGAAAGGGGTCTCCCAAGGCCAGAGGTCCGGCTGCCAGTCCCGATCAGAT 1326
Qy 1257 --CGAGGGAGTCCACCAAGTGCAGAAAGCTGAGCTTCAACGACGAAACCGCTTC 1314
Db 1327 CTGTATGACAGCCCAAGCAAGGTGCCAAGAGCTGTGAGCTTGTGTGACCCGACGCCACA 1386
Qy 1315 CGGCTCTGCTGCGCTCAAAAGTTCTCAGCCAAAACAGTATAGATGTGACACAGCC 1374
Db 1387 CGCAGAGCTTTCGCGATCAAGGGTGTGATCCCGCAGAAATTCAGAAAGAGCCCTC 1446
Qy 1375 CTGTGACATGATGATATATGATGAAAAAGATGCGAGTGTATCAGTGGAAAGC 1434
Db 1447 CCTGGGAGAGATCTGTAGAGACAAAGAGCTGAGAGTTTGTGACTGAGAT 1506
Qy 1435 CTCACCCCAACATTTAAATGTGATTCGAGCTATCAGAAATTAAGAAATTTTCATGTGGA 1494
Db 1507 CTTACCCCTGGCTCAAAATGATGATCAGAGCCGTGTGTATGTGGGTTCTTGGTATCT 1566
Qy 1495 AAACGGAAGTTTAAAGAAAAGTTACGTTCATATGATGTAAAGATGTCAATGGAACATAT 1554
Db 1567 AAGCGAAAGTTCAAAAGAGTCTGCGCCCATATGATGTATGGAAGCTCATCGAAAGCTAC 1626
Qy 1555 TCTGCTGTGATGTGACATGTGTGTGTAATTAAGGCTTCAACACAGTGTGATCA 1614
Db 1627 TCGGTGTGACACTTGTGATATGTTGTCCCGATCAAGAGCTGTGAGACGAGTGGACG 1686
Qy 1615 ATTCTTGAAAAGGGGCAATTCATCAGATTAAGAAAGCGAGAGAAAATTAACAGCAGA 1674
Db 1687 ATTGTGGGGCGGGGCCCAACATTAACGATTAAGAA---TCGACCAAAAGGCCACGGGAA 1743

Qy 1675 CATGAGACCAGACATCTGATGCTCGGTGGGTGTCAAGTTGAAAAACAGTA 1734
Db 1744 ACGAGAGTCCCGAAGAACCCACGATGATGGAGCGCTTGGGAAGGTGAGAAACAGGTC 1803
Qy 1735 CAGTTCATAGAGTCCAACTGAGTCTGCTACTAGACATCTATCAACAG 1782
Db 1804 TTGTCCATGAAAAAGAAAGTCCGACTTCTTGGTGAACATCTATACAG 1851

RESULT 8
US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanz, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22

Query Match 18.9%; Score 510; DB 3; Length 2169;
Best Local Similarity 58.1%; Pred. No. 3.9e-141;
Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;

Qy 64 GGCCTGCTACTGCTGAGGACCGCGGCGCAAGCTTGTGTGGGCGGGGAGCTGAG 123
Db 67 GCTTGTGTGGGCTGTGACCCCGCGCGCTCACTCAACGCGAGCGGCTTACTATC 126
Qy 124 GAGAGCCCGCGGCGCAGAGGGGCGCGATGAGCTGTGGGAAACCGCTCTTTAC 183
Db 127 GCGGCTCCGAGGCGCCCAAGCGGCGAGCGTTTGAAGAACCGGAGCGGCGG 186
Qy 184 ACGATACCCAGAGTGTCCGCGCGCAAGTCAAGTACCGGCGGTGCAAACTACCTGAC 243
Db 187 GAGCGCGGAAAGCCCGCAAGCGCAACGCTTTTACCGCAAGCTGCAAAATTTCTCTAC 246
Qy 244 AACGTGTGAGAGAACCCCGCGGCTGAGCTTCAACAGCTTGTGTTTCTCTCT 303
Db 247 AACGTGTGAGAGCGGCGCCCGCGGCTGAGCTTCAACAGCTTGTGTTTCTCTCT 306
Qy 304 GTCTTTGCTGCTGATTTTGTGATGTTTCTTACATCTTGAACACAAATTTGCGC 363
Db 307 GTCTTCTCTGCTGCTGCTTCTTGTGTTTTCACCATCAAGAGTACAGAAAGCTCT 366
Qy 364 TCAAGTCCCTCTGATCTCTGAGTGTGATGATGTGTGCTTGTGTTGAGATTCATC 423
Db 367 GAGGGGCGCTTCAATCTTGAATTTGAAATCTGATCTATCTGATGATGATGATCTTT 426
Qy 424 ATTCAATCTGATCTGCGGCTGCTGTTGTGATATAGAGATGAGCAAGAACTGAG 483
Db 427 GTGAGATCTGGGCTGCGAGGCTGCTTGTCCGATTCAGAGCTGAGAGGCGAGCTCAAG 486
Qy 484 TTTGCTGAAAAGCCCTTGTGTGATATAGATCAATTTGTTATGCTTCAATAGCACT 543
Db 487 TTTGCAAGAAAGCGTCTGTGTGATGATATCATGTGTGATTTGCTCCATTTCTGTG 546
Qy 544 GTTTGTGAAAACCTCAGGGATATATTTTGTGCAAGTCTGACATCAAGATCTCCGTTTC 603

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Db 547 CTGGCTCTGGTTCCTCCAGGGCAATGTCTTGGCAGCATCTCGGCTCGGACTTGGGGTTC 606
Qy 604 CTACAGATCTCTCCGATGTCGCGATGAGACCGAAGGGGAGGACCTTGGAAATTAAGTGGT 663
Db 607 TTGGAAATCTTGGGATGATCCGTATGACCGGAGGGGTGGCACCTGGAAAGCTTGGGA 666
Qy 664 TCAGTGTATGCTCAACAGAAATTAATCAAGCTTGTATCAATAGGATTTTGGT 723
Db 667 TCGGTATCTACGCTCAACAGAAAGACTGGTGTATCTCGGTATCAATGGCTTCTCTGC 726
Qy 724 CTATTTTTCGTTCTTCTTCTTCTATCTGTGTGAAAAAGATGCCAATAAAGTTTCT 783
Db 727 CTGATCTGGCTCATTTCTGTGTATCTGTGCAAAAAAGGTGAATGACCACTTGGAC 786
Qy 784 ACATATGCAATGCTCTCTGTGGGGGCACAATTAATGACCAATATATGCTATGAGAC 843
Db 787 ACCTAGCGAATGACATCTGTGGGGGTGTATCACCTGACGACATTTGCTACGGGGAC 846
Qy 844 AAAACTCCCTTAATCTGGCTGGGAAAGATGCTTTCTGACGGCTTGGACCTCTGGCAT 903
Db 847 AAGTACCTCTAGACCTTGGAAACGGAGGCTCTGGCAGACCTTTACCTCATTTGCTC 906
Qy 904 TCTTTCTTGGACATTCCTGCGGCAATCTTGGCTCAGGTTTTCATTTAAAGTACAAGAA 963
Db 907 TCGTTCTTCTCTCTCTGCTGGCATTTTGGATCCGGCTTTGCGCTGAAAGTCCAAGAG 966
Qy 964 CAACACCGCCAGAAACCTTTGAGAAAAAGAAAGAACCCAGCTCCAACTCATTCAGTCT 1023
Db 967 CAGATCTGGAAAAACCTTTGAGAAACGGGGAACCTTGGCAGGTCTGATTCAGTCT 1026
Qy 1024 GTTTGGCGTATTAACGAGCTGATGAGAAAT----- 1054
Db 1027 GCCTGAGATTTCTATGCTATTAACCTCTACGACCGACCTGACCTCACTGAGCAGTAC 1086
Qy 1055 -----CTGTTTCATTGCAACTGGAAGCCACACTTGAAGCCCTTGAC 1098
Db 1087 TACGAGCGACAGTCACTGTCCCATGTACAGACTCATCTCCACTGGAACAGCTGGAG 1146
Qy 1099 ACCTGCAGCCCTACCAAG-----AAGAACAGGGGAA 1131
Db 1147 CTGCTGAGGAATCTCAAGAGCAAAATCGACTCACTTCAGAAAGGACCAAGCAGAG 1206
Qy 1132 GCATCAGCAGTCAAGAGTAAATTTAAGAGGAG-----TGCGCATGCTAGCCCAAG 1188
Db 1207 CCACTACCAAGTCAAGAGTCAATTTGAAGATCGTCTTCTTCAGGCCCCAGAGCATG 1266
Qy 1189 GGGCAGATTTAAGAGCCGACCAAGCCTCACTAGTGAAGAGGTTCCCAAGCAGCAG 1248
Db 1267 GCTGCCAAGGAAAGGGGTCTCCCAAGGCCAGACGGTCCGGGGTCCCAAGTGGGAA 1326
Qy 1249 ATACAGACCGAGGCACTCCCAACCAAGTCAAGAGCTGAGCTTCAACGACCAAGC 1308
Db 1327 CAGAGTCTGTATACAGCCCGACCAAGGTGCCCAAGCTGAGACTTTGTGACCCGAG 1386
Qy 1309 CGCTTCGGGCTCTCGCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGAC 1368
Db 1387 CGACACGCGAGGCTTCCGATCAAGAGTCTGATCCGCGAGAAATTAAGAGCAAGC 1446
Qy 1369 ACAGCCCTTGGCACTGATGATATGATGAAAAAGATGCCAGTGTATGATCAAGT 1428
Db 1447 C---TCCTGGGAGGAGCATGTAAGAGCAACAGAGCTGTAAGTGAAGTTTGAAGT 1503
Qy 1429 GAAGACTCACTCCCACTTAACCTGTATTCGAGCTTCAAGAAATTAAGAAATTTCA 1488
Db 1504 GAAGATCTTACCTCGCTCAAGAGTGAAGTCAAGAGCTGTGTGTATGACGGTCTTGG 1563
Qy 1489 GTTGCAAAAAGAGTGAAGAAAGTTCAGTCAATGATGTAAGAAAGTCAATGAA 1548
Db 1564 GTATCTAAGGAAAGTTCAAAGAGAGTCTGCGCCATATATGATGAGCGTCAATGAA 1623
Qy 1549 CAATATTCGTGCTGCTATCTGAGCATGTTGTGAAATTAAGACCTTCAACACGTTGT 1608
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Db 1624 CAGTACTCGGCTGAGCACTTGATATGTTGCCGATCAAGAGCCTGCACTCAGAGTG 1683
Qy 1609 GATCAATCTTGGAAAAAGGCAATTCACATCAGATTAAGAGCCGAGAGAAATTAAGA 1668
Db 1684 GACCAATTTGGGGCGGGGCCCAACAAATTAAGATTAAGAA--TGCACAAAGGCCCA 1740
Qy 1669 GCAGAAATGAGACACAGACGATCTCAGTATGCTCGTGGGTGTCAAGTTGAAAAA 1728
Db 1741 GCGGAAAGGAGCTGCGGAGAGACCCACAGATGATGAGAGCGCTTGGAAAGTGGAGAA 1800
Qy 1729 CAGGTACGTCATAGAGTTCAGAGCTGAGCTGCTATCTAGACATCTATCAACAG 1782
Db 1801 CAGGTCTGTCCATGAGAAAGAGCTGACTTCTGTGTGAGCATCTATACAGAG 1854
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RESULT 9
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Yang, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495, 050A
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303
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Query Match 18.9%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.8e-141;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1621 GAAAAAGGCAATATCAATCAATTAAGAGAGCCGAGAAAAATTAACAGACAACTGAG 1680
Db 1 GAAAAAGGCAATATCAATCAATTAAGAGAGCCGAGAAAAATTAACAGACAACTGAG 60

Qy 1681 ACCACAGAGATCTAGATGCTCGGTGGGTGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db 61 ACCACAGAGATCTAGATGCTCGGTGGGTGTCAAGGTTGAAAAACAGGTACAGTCC 120

Qy 1741 ATGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGATCTTCGAAAGGCTCT 1800
Db 121 ATGAGATTCAGCTGAGCTGCTTACTAGACATCTATCAACAGATCTTCGAAAGGCTCT 180

Qy 1801 GCTCAGCCCTGGCTTGGCTTCAATCCAGATCCCACTTTGAAATGAAAGACAGATCT 1860
Db 181 GCTCAGCCCTGGCTTGGCTTCAATCCAGATCCCACTTTGAAATGAAAGACAGATCT 240

Qy 1861 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCGCAAAACAGTGGCTGC 1920
Db 241 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCGCAAAACAGTGGCTGC 300

Qy 1921 TTATCCAGATCAATGATGCAACATCTCGAGAGGCTGCAATTTCTGACGCCAAT 1980
Db 301 TTATCCAGATCAATGATGCAACATCTCGAGAGGCTGCAATTTCTGACGCCAAT 360

Qy 1981 GAGTTCAGTCCCAAGCTTTCAAGCGCTTACCCCTATCATGACAGTCAACAGACAG 2040
Db 361 GAGTTCAGTCCCAAGCTTTCAAGCGCTTACCCCTATCATGACAGTCAACAGACAG 420

Qy 2041 GTGCCAATTAATCAAGAGGATGCTCAGCATGTGGAGGCCAACACCAATGGCAACCA 2100
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QY 195 GAGCTGCG-----GGCGAAGCTCAGATACCGGCGGGTGAGAGAACTACTGTGACA 245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 474 GAGCCGCCCAAGTCAAGAGAAACAGCCCAAGTACAGGCGATCCAACTTATCTATGA 533
QY 246 CGTGTGAGAGACCCCGCGGCTGGGCGTTCATCTACACGCTTGTGTTTCTCTGTG 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 534 CGCCCTGGAAGACCGCGGGGCTGGGCGTGTCTACAGGCGCTGTGTCTGTATTTGT 593
QY 306 CTTTGTGTGTTTGTATTTTGTCACTGTGTTTCTACATCCCTGAGACACAAATTTGGCCTC 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 594 CTTGGGATGTCTATTTCTGCGCGGTCTACACCTTCAAGAAATATGAGACTGTGTCTG 653
QY 366 AAGTTGCGCTTGTATCTGTGAGATTCGTGATGATTCGTGTTTGTGGATTCATCAT 425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 654 AGCTGCGTTTCTGTCTGAAACATTTGCTATTTTCTATTTTGAAGCTGAGTTGCTTT 713
QY 426 TCGAATCTGTCTGCGGTTGCTGTGTCATATAGAGATGCGAAGAGACTGAGATT 485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 714 GAGGATCTGGGCTGAGAGATGTTGCTGTGATCAAAAGCTGGCGTGAAGCTTAAAGTT 773
QY 486 TGTCTGAAAGCCCTTCTGTGTATATGATACCATTTGTTTATGCTTCAATAGCAATTGT 545
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 774 TGCAGAGAAAGCCCTGTGCAATGTTGACATCTTGTACTGATTCCTGTGTCCAGTGTGT 833
QY 546 TTCTGCAAAAACACAGGCTAATATTTTGTGCAAGTGTGCACTGAAAGTCCGTTTCC 605
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 834 TCCCTGGGAAACAGAGGCAATGCTTGGCCACT--CCCTCGAAGCCTTGTGCTTCT 890
QY 606 ACAGATCTTCGCGATGATGTCGATGAGACCGAAGGGAGGCACTTGGAAATTAATGAGTTT 665
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 891 GAGATCTGCGCATGCTTGAATGATAGAGGGGTGGGCACTGGAAGTCTCTGGGCTC 950
QY 666 AGTGGTTTATGCTCAAGCAAGAAATTAATCACAGCTTGTATATGATTTTGTCT 725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 951 GGTATCTGTGCCCACAGCAAGAACTCATCACTGCTGTATCATGAGTGGCTTCTGACAT 1010
QY 726 TATTTTGTGCTTCTGCTGTCTATGCTGTGAAAGATG-----766
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1011 CATCTTTTCTTCACTTTTGTCTACTGATGAGAAAGATGTCCGAAATGGAATCCCA 1070
QY 767 -----CCAAATAAAGATTTTCTACTATGAGATGCTCTGTGTGGGCAAT 815
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1071 AAGAGAGAGATGAAGAGAGATTTAGAGCTATGAGAGTCTGTGTGGGCGCTGAT 1130
QY 816 TACATTGACACTATTTGGCTATGAGACAAACTCCCTTACTTGTGCTGGAAAGATTGCT 875
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1131 CACACTGGCCACCATTTGTATGAGACPRAGACACTAAACCTGGGAAAGAGCTCTGAT 1190
QY 876 TTCTGAGGCTTGGCACTCCTTGGCAATTTCTTCTTGTGCACTTCGCGGGCAATTCCTGG 935
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1191 TGTCTGCACCTTTTCTTAAATGCGCGCTCTCTTTTGTGCTTCCGAGAGCACTTGG 1250
QY 936 CTCAGGTTTTGCAATTAAGTACAGAACACCGCCAGAAAACATTTGAGAAAAGAG 995
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1251 CTCAGAGACTGGCACTGAAGTTTCAAGAGAGACGCGTCAAGAACACTTTGAGAAAGAG 1310
QY 996 GAAACCAAGCTGCCAATCTTATTAAGTGTGTTTGGCGTATGACGAGCTGATGAGAAATC 1055
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1311 GAAGCCAGCTGCGAACTCATTCAGGCTGCTGGAATATTAATGATCAACACCCCAACG 1370
QY 1056 TGTTCATTTGCAACCTGGAAGCCACACTTGAAGGCTTGACACCTGACGCTTACAA 1115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1371 GTTGAATCTGTGTGCAACTGAGATCTTAATGATCAATGTTGTCTTTTCCATTTCTTCA 1430
QY 1116 GAAAGAACAGGGGAAAGCATCAAGAGTCAAGAGTTTAAAGTGAAGAGATGCGCAT 1175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1431 GAAAGAACAACTGGAAGACAGACAGCCAAAGTGGGCTCTGTGATCGGGTTGCGCT 1490
QY 1176 GGTACGCCCAAGGGGCAAGATTTAAAGCCGACAAGCTCAATGATGATGAGAGAGATC 1235
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Db 1491 TTCTAATCTCTGATGAGCAATTA-----AGAAAGCTATTTAC 1532

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QY 1236 CCCAAGCAGCATCATCAAGCCGAGGCGAGTCCCAAAAGTGAAGAGCTGAGCTT 1295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1533 CCTCTGAATGTAGATGCTATGAAAGAAAGCCCTTCCAAAGGCCAAAGCCTTGGCTT 1592
QY 1296 CAACGACCGAACCCGCTTCCGCGCCTCGCTGCGCTCAAAAGTTCTCAGCCAAACCACT 1355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1593 AAACATATAAGAGCGTTTCCGACCGGCTTCCGATGAAAGGCTACGCTTCTGCGAGAG 1652
QY 1356 GATAGATGCTGACAGACGCTTGGCACTGATATGATATATGATGAAAGATGCCAGTG 1415
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1653 WTCTGAAGATGCTGGGACAGGCGACCC-----CATGGCAGAAGCAAGGGGCTATGGGA 1706
QY 1416 TGATGATCAGTGAAGAGACTCACCCACACTTAAATCTGATTCGATCGATCGAAT 1475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1707 TGAATCTCTCATTAAGACATATGCTTCCTTAAAGCTGCGATCCGAGCTGTGAGAT 1766
QY 1476 TATGAATTTCAATGTTGCAAAAAGAGTTTAAAGAAAGTTACGTCCATATATGTA 1535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1767 TCTACAGTTCCGCTCATATATAAATAAAAGTTCAAGAGAGAGCTTGAAGCTTATGATGTA 1826
QY 1536 AGATGCTATTGAACAATATTTCTGTGTGATCTGACATGTTGTGTAATAAAGCT 1595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1827 AGATGATTTGACAGTATTTGGCCGGAATCTTGAATGCTTTCAAGATTAAGTCT 1886
QY 1596 TCAACAACGTGTTGATCAATTTCT 1619
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1887 ACAGACAGAAATGATATGATTTT 1910

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RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamir, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gridkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIORITY FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

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Query Match      17.1%; Score 460.8; DB 3; Length 2565;
Best Local Similarity 57.9%; Pred. No. 2.2e-126;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

QY 13 GAGTGGGCGGGGAGAGGTTGCTGTAATTCGAGAGCGCCAGGAGCGGCTGTGA 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 GGGGGGGGGCGGGGAGAGAGGAGGAAAGGGGGCTGGGCGCCGGGAGCGTGAAGCAA 102
QY 73 CTGTGTGGGACCCCGCGCGCCACGCTTGATGCGCGCGCGGTGCTGAGAGAGAGCCGC 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 GTCACTTTGGCCCTCGGGGCGAGACCGAACAGGAGACCTTGCTCTGTGAGGGCGCG 162
QY 133 CGGGGCAAGCAGGGGCGCCGATGAGCTGTGGGAAAGCCGCTCTTACAGAGTGAAC 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 GCGCGGACGAGGGGCGAGGAGAGACCCGACAGGAGATCGGCTCTTGAGCCAAAGCCCCG 222
QY 193 CAGAGCTGCG-----GGCGAAGCTCAAGTACCGGCGGGTGAGAACTAATCTGTAC 243
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Db 223 CTGAGCGCCCGAGTCAAGAAACAAGCCAGATCCGGCGATCCAACTTTGATCTAC 282
QY 244 AACGTCGTGAGAGAGAGCCCGCGGCTGAGGCTTCATCTACACGCTTTCGTTTCTCTT 303
Db 283 GAGCGCTGAGAGAGAGAGCGGGGCTGGGCGCTCTTACACCGCTTGGTTCGATTT 342
QY 304 GTCTTTGTTGCTTGAATTTTGTCAAGTCTTCTACATCTCTGAGCAACAATAATGGCC 363
Db 343 GCTCTGGGGGTGCTTGTGCTGTCTGACCACTTCAAGAGATATAGACTGTCTGTG 402
QY 364 TCAAGTTGCTCTGTATCTGAGAGTCTGATGATGTGTGCTTGTGAGTTCATC 423
Db 403 GAGAGCTGCTCTGTATCTGAGAGATTTGCTATTTTATCTTGTGAGCCGATTTGCT 462
QY 424 ATTGATCTGTGCTGCGGCTGCTGTTCATATAGAGATGCGAGAGAACTGAG 483
Db 463 TTGAGAGATCTGGGCTGCTGATGTTGCTGCGATACAAAGGCTGGGGGCGAGCTGAG 522
QY 484 TTTGCTGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCAT 543
Db 523 TTTGCGAGAGAGCCCTGTGATGTTGACATCTTGTGCTGATGCTCTGTGCGCAGTG 582
QY 544 GTTTCGCAAAAAGCTAGGGTATATTTTGCAGCTGCACTGCAAGTCTCCGCTTC 603
Db 583 GTTGTGAGAGAAACCAAGCAATGTTCTGGCCACTT---CCCTGCAAGCCCTGGCGTTC 639
QY 604 CTACAGATCTCTCGCATGCTGCGATGACCGAAGGGAGAGCACTTGAATTTACTGGGT 663
Db 640 CTGCAAGATCTGTGCGCATGCTGGGAGATGAGCCGAGAGAGTGGACCTTGGAAGCTTGGGCG 699
QY 664 TCAGTGTGTTATGCTCAAGCAAGAAATTAATCAAGCTTGGTCAATAGATTTTGGTT 723
Db 700 TCAGCATCTGTGCGCACAGCAAAAGCATCATCAGCGCTGGTATCATCGTTTCTCGACA 759
QY 724 CTATATTTTTCGCTTCTCTGTCTATCTGTGAGAAAGAGTGC-----768
Db 760 CTCATCTCTTCTTCAATTTCTGTCTACCTGTGTGAAGAAAGCTCCCAAGGTGATGCA 819
QY 769 -----AATAAGAGTTTCTACATATGACAGATGCTCTGTGTGGGACACA 813
Db 820 CAAGGAGAGAGATGAAGAGAGGTTGAGACCTATGAGATGCTCTGTGTGGGCGCTG 879
QY 814 ATTACATTGACAACTATTGGCTATGAGAGCAAACTCCCTTAACTTGGCTGGAGATTG 873
Db 880 ATCACTGCTGCGCACATGCTATGAGACCAAGACCAACCAAAACGTGGAGAGCGCTCTG 939
QY 874 CTTTTCGAGAGCTTGCATCTCTGCTGCTTCTTCTTGTGCACTTCTGCGCGCATCTT 933
Db 940 ATTGCGGCACTTCTTCTTAAATTTGGCGTCTCTTCTTGTGCGCTTCTGAGCGGCGATCTG 999
QY 934 GGCCTCAGTTTTCATTAAAGTACAAAGAACACCGCCAGAAACATTTTGAGAAAGA 993
Db 1000 GGGTCCGGGCTGGCCCTCAAGGTGAGAGCAACCGTCAAGAGACCTTTGAGAAAAAG 1059
QY 994 AGGAAGCCAGCTGCCAATCTATTCACTGTGTGTTGGCGTATGTTACCGACGTGAGAAA 1053
Db 1060 AGGAAGCCAGCTGCTGAGCTCAATTCAGGCTGCTGAGGTATATGCTCAACACCCCAAC 1119
QY 1054 TCTGTTTCATTCAGCAACCTGGAAGCACACTTGAAGGCTTGAACACCTGAGCCCTTAC 1113
Db 1120 AGGATTTGACTGGTGGCGACATGAGATTTTATGATTCAGTGTCTCTTCTTCTTCTTTC 1179
QY 1114 AAGAAAGAACAGGGAGACATCAAGCAGTCAAGAACTAAGTTTAAAGAGGAGTGCAGC 1173
Db 1180 AGGAAAGAACAGTGGAGGAGCATCAAGCAAAAGCTGGGTCTCTTGAATGGGTTCGC 1239
QY 1174 ATGGCTAGCCCAAGGGGCGAGAGTATTTAAGCCGACAAAGCTCAATAGTGAAGAGAG 1233
Db 1240 CTTTCTAATCTCTGTGTAGCATATAA-----AGGAAAGCTATTT 1281
QY 1234 TCCCAAGAGACGACATCAAGCCGAGGCGACATCCCAAAAGTGAAGAGAGCTGAGAC 1293
Db 1282 ACCCTCTGATGTAGATGATGATGAAGAAAGTCTTCTTAAAGAACCAAGGCTGTGGC 1341

QY 1294 TTCAACGACCGAACCCTTCGCGCTCGCTGCGCTCAAAAGTTCTCAGCCAAACCA 1353
Db 1342 TTAAACATTAAGAGCGTTTCGACAGCGCTTCGCGCATGAAAGCT-----ACGCTTTC 1395
QY 1354 GTGATAGATGCTGACACAGCCCTTGGCACTGATGATGATATGATGAAAGAAAGATGCCAG 1413
Db 1396 TGGCAGAGTTCTGAAGATGCCGAGCAGGTGACCCCATGGCGGAGAGACAGGGGCTATGGG 1455
QY 1414 TGTGATGATCAGTGGAGAGACCTCACCCACACTTAAGCTGTGATTCGAGCTATCAGA 1473
Db 1456 AATGACTTCCCATGGAAGACATGATCCCACTGAAAGCCGCGCATCCGAGCCGTACGA 1515
QY 1474 ATTATGAATTTCAATGTTGCAAAACGAAAGTTTAAAGAAAGTTACGTCATATGATGTA 1533
Db 1516 ATTCTACAAATTCGCTCTCTATTAAGAAATTTCAAGAGAGACTTTGAGGCTTACGATGTG 1575
QY 1534 AAAGATGATTTGAACATATTTGCTGCTGCTCATCTGCAATGTTGTATGAAATTAAGAC 1593
Db 1576 AAGATGTGATTTGAGCAGATATTTGCGCGGCACTTCGACATGCTTTCAGAGATTAAGTAC 1635
QY 1594 CTTCAACACGTTGATCAAAATCT 1619
Db 1636 CTTCAACGACGATATGATATTTT 1661

RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Lepert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
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NAME/KEY: unsure
LOCATION: 486, 510, 552, 573
OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

Query Match 16.8%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 3,2e-124;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

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Sequence 19, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blauar, Michael A.
APPLICANT: Dworesky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neuberger, Michael G.
TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105, 058C
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
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ORGANISM: Homo sapiens
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Best Local Similarity 64.7%; Pred. No. 1.3e-115;
Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

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Job time : 307.493 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 2694

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Gapop 10.0 , Gapext 1.0

Searched: 9772231 seqs, 4124568258 residues

Total number of hits satisfying chosen parameters: 19544462

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Listing first 45 summaries

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SUMMARIES

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5	2689.2	99.8	3137	19	US-10-661-629-1
6	2681.2	99.5	3074	9	US-09-813-148-1
7	2681.2	99.5	3074	21	US-10-399-489A-5

8	2679.6	99.5	3074	21	US-10-482-834A-55	Sequence 55, Appli
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19	510	18.9	2169	13	US-10-131-685-22	Sequence 22, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, JOANNE T
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIORITY FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Patent No. US2002010267A1
; GENERAL INFORMATION:
; APPLICANT: Jogle, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US2002010267A1e1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Query Match 100.0%; Score 2694; DB 9; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGATGTGAGTGGGCGGAGGAGGAGTGTCTGTAATCTCGAGCGCGCAAGGAGC 60
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QY 301 CTGTGCTGTGTGCTTGAATTTTGTGAGTGTCTTACCATCCCTGAGACACAAATTTG 360
DB 301 CTGTGCTGTGTGCTTGAATTTTGTGAGTGTCTTACCATCCCTGAGACACAAATTTG 360
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QY 421 ATCATTCGAATCTGATCTGCGGGTTGCTGTTCGATATAGAGATGAGCAAGAGACTG 480
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DB 481 AAGTTTGTCTGAAGCCCTTCTGTATATAGATACCATTTGTTCTTATCGCTTCAATAGA 540
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DB 541 GTTGTCTTGCAGAAAAGCTCAGGGTAATATTTTTCAGAGCTTCGACTCAGAACTTC 600
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RESULT 3
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US2005006491A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCMOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-493-1

Query Match 100.0%; Score 2694; DB 21; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGATGTGAGTTCGCGCCGCGGCAAGGTTGCTGAACTCGGACCGCGCAGGCG 60
Db 1 ATGAAGATGTGAGTTCGCGCCGCGGCAAGGTTGCTGAACTCGGACCGCGCAGGCG 60
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Db 121 AGGAGAGCGCGCGGCGCAAGAGGAGGCGCGGATGAGCTGTGGGGAAGCGGCTCT 180
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Db 1921 TTAATCCAGATCAATATGTGCAACATCTGAGAGGCTTGCAGTCAATTTGACGCCAAT 1980
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Db 2521 GTGGGTCCTCGAAGACAGACAGACACTTTTGATGCGGACCGAGCTTCCAGGAA 2580
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Db 2581 GGTGCTTTGCATCAACTCTCTAAGGACTGGAAGGTACGATCATCTGAGCATTTGT 2640
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RESULT 4
US-09-810-796-1

; Sequence 1, Application us/09810796

; Patent No. US20020102677A1

; GENERAL INFORMATION:

; APPLICANT: Jogle, Timothy James

; APPLICANT: ICAGEN, Inc.

; TITLE OF INVENTION: KCN05, a No. US20020102677A1 Potassium Channel

; FILE REFERENCE: 018512-005010US

; CURRENT APPLICATION NUMBER: US/09/810, 796

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: US 60/190, 954

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 1

; LENGTH: 3071

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human outwardly rectifying, voltage-gated

; OTHER INFORMATION: potassium channel KCN05-1

; NAME/KEY: CDS

; LOCATION: (10)..(2703)

; OTHER INFORMATION: KCN05-1

; US-09-810-796-1

Query Match 99.9%; Score 2690.4; DB 9; Length 3071;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGATGTGAGTCGGGCGGAGGCAAGGTCCTGTAACCTCGGACGCGCAAGGAGC 60
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Db 10 ATGAAGATGTGAGTCGGGCGGAGGCAAGGTCCTGTAACCTCGGACGCGCAAGGAGC 69
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Db 70 GACGCGCTCTACTGCTGGGACACCGCGCGGCAACGCTTGTTGGGCGGCGGTCGCTTG 129
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Db 190 TACACGAGTAGCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGAGTGAAGACTTACCTG 249
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Db 250 TACAAAGTCTGAGAGACACCGCGGCTGGGCTTATCTACACGCTTTGTTTTCTC 309
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Db 310 CTGTGCTTGGTGTGATTTTGTCACTGTTTCTTACCATCCCTGAGACACAAATTTG 369
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Db 370 GCTTCAGTGGCTCTTGATCTCGAGTTCGTGATGATTTGTCTTTGTTGGATTC 429
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Db 790 TCTACATATGAGATGCTCTCTGTGGGGGACAAATTAATTGACAACTATTTGGCTAT 849
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QY 841 GACAAAACCTCCCTTAACCTTGGCTGGGAAGATTGCTTTGCAAGGCTTTCACCTCTTGGC 900
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RESULT 5
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNE
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1
Query Match 99.8%; Score 2689.2; DB 19; Length 3137;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY	1441	CCACCACTTAAACCTGTCATTTCGAGCTATCAGAAATTATGAATTTTCATGTTGCAAAACGG	1500
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QY	1561	GGTCATCTGGACATGTTGTGTGAAATTTAAAGCCTTCAACACGCTTTCATCAAAATTCCTT	1620
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QY	1681	ACCAACAGCGATCTCAATGATCTCGGCTCGGCTGGTCAAGGTTTGAAGAAAACAGTACAGTCC	1740
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Db	2015	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT	2074
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Db	2195	GAGTTCAGTGGCCCGAGACTTTTCTAAGCGCTTAAGCCCTACTATGCAACTCMAAGCAACAG	2254
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Qy	2161	GCCATCAAGCATCTGCCAGGCGCCAGAAACTCTGCACTTAACCTCGAGGCTTACAGAA	2220
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Qy	2221	AGCATTTCTGACGTCACACCTGCTGTGGCTTCCCAAGGAAATGTTTCAGGTTGACAG	2280
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RESULT 8			
US-10-482-834A-55			
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: Publication No. US2005074764A1			
: GENERAL INFORMATION:			
: APPLICANT: Mulley, John Charles			
: APPLICANT: Harkin, Louise Anne			
: APPLICANT: Dibbens, Michelle			
: APPLICANT: Wallace, Robyn			
: APPLICANT: Phillips, Hillary Amy			
: APPLICANT: Heron, Sara Elizabeth			
: APPLICANT: Berkovic, Samuel Frank			
: APPLICANT: Scheffer, Ingrid Eileen			
: APPLICANT: Bionomics Limited			
: TITLE OF INVENTION: MUTATIONS IN ION CHANNELS			
: FILE REFERENCE: 1386/17			
: CURRENT APPLICATION NUMBER: US/10/482.834A			

/ CURRENT FILING DATE: 2004-01-02
 / NUMBER OF SEQ ID NOS: 173
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 55
 / LENGTH: 3074
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-10-482-834A-55

Query Match 99.5%; Score 2679.6; DB 21; Length 3074;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2685; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	1	ATGAAGATGTGAGTCGGGCGGCGGCGAGGTCCTGTAACCTCGGCGAGCGCGAGGCGC	60
Db	215	ATGAAGATGTGAGTCGGGCGGCGGCGAGGTCCTGTAACCTCGGCGAGCGCGAGGCGC	274
Qy	61	GACGGCTGTACTGCTGGGCACTCCGCGGCGGCGAGCTGTGGCGGCGGCGGCTG	120
Db	275	GACGGCTGTACTGCTGGGCACTCCGCGGCGGCGAGCTGTGGCGGCGGCGGCTG	334
Qy	121	AGGAGAGCGCGCGGCGGCGAGCGGCGGCGGAGTGAAGCTGTGGGGAAGCGCTCTCT	180
Db	335	AGGAGAGCGCGCGGCGGCGAGCGGCGGCGGAGTGAAGCTGTGGGGAAGCGCTCTCT	394
Qy	181	TACACGATAGCCAGAGCTGCGCGCGCAACGTCAAGTACCGCGGCGGCGAGACTACCTG	240
Db	395	TACACGATAGCCAGAGCTGCGCGCGCAACGTCAAGTACCGCGGCGGCGAGACTACCTG	454
Qy	241	TACACGCTGTGAGAGACCCCGCGGCTGGGCGTTCATCTACCAAGCTTTGTTTTCTC	300
Db	455	TACACGCTGTGAGAGACCCCGCGGCTGGGCGTTCATCTACCAAGCTTTGTTTTCTC	514
Qy	301	CTTGCTTTGGTGTGATTTTGTCAAGTGTTCATCCATCCCTGAGACAATAATTG	360
Db	515	CTTGCTTTGGTGTGATTTTGTCAAGTGTTCATCCATCCCTGAGACAATAATTG	574
Qy	361	GCCTCAAGTGGCTCTTGAATCTGAGATTCTGATGATTTGCTCTTTGGTTGAGTTC	420
Db	575	GCCTCAAGTGGCTCTTGAATCTGAGATTCTGATGATTTGCTCTTTGGTTGAGTTC	634
Qy	421	ATCATTCGAAATCGATCTCGGAGTGTCTGTTCATATAGAGATGCGAAGAACTG	480
Db	635	ATCATTCGAAATCGATCTCGGAGTGTCTGTTCATATAGAGATGCGAAGAACTG	694
Qy	481	AGGTTGCTCGAAGCGCTTGTATAGATACATTTCTTACGCTTCAATAGCA	540
Db	695	AGGTTGCTCGAAGCGCTTGTATAGATACATTTCTTACGCTTCAATAGCA	754
Qy	541	GTGTTTCTGCAAAAATCAGGGTAATATTTTTCACAGCTTGCACCTGAAATCTCCGT	600
Db	755	GTGTTTCTGCAAAAATCAGGGTAATATTTTTCACAGCTTGCACCTGAAATCTCCGT	814
Qy	601	TTTCCTACAAATCTCTCGCATGTGGCGCATGACCGAAGGGAGGCACTTGGAAATTAAGT	660
Db	815	TTTCCTACAAATCTCTCGCATGTGGCGCATGACCGAAGGGAGGCACTTGGAAATTAAGT	874
Qy	661	GGTTCAGTGTATGCTCAACAGAGAAATTAATCAAGCTTGGTACATAGAAATTTTG	720
Db	875	GGTTCAGTGTATGCTCAACAGAGAAATTAATCAAGCTTGGTACATAGAAATTTTG	934
Qy	721	GTTCCTAATTTTTCGTCTTCTGTCTATCTGGTGAAGAAAGATGCCAATAAGATT	780
Db	935	GTTCCTAATTTTTCGTCTTCTGTCTATCTGGTGAAGAAAGATGCCAATAAGATT	994
Qy	781	TCTACATATAGAGATCTCTGTGTGGGCGCAATTAATGAATTAATTTGGCTATGGA	840
Db	995	TCTACATATAGAGATCTCTGTGTGGGCGCAATTAATGAATTAATTTGGCTATGGA	1054
Qy	841	GACAAAATCTCCCTTAATCTGGCTGGGAAATTTGCTTTCGAGGCTTTGCACTCCCTGGC	900
Db	1055	GACAAAATCTCCCTTAATCTGGCTGGGAAATTTGCTTTCGAGGCTTTGCACTCCCTGGC	1114

Qy	901	ATTCTTTCTTTGCACTCTCTCCGCGATTCCTGGCTCAGGTTTGTGATTAAGTACAA	960
Db	1115	ATTCTTTCTTTGCACTCTCTCCGCGATTCCTGGCTCAGGTTTGTGATTAAGTACAA	1174
Qy	961	GAAACAACCCGCGAGAAACATTTGAGAAAAGAGAAACCCAGCTGCCAATCTTACG	1020
Db	1175	GAAACAACCCGCGAGAAACATTTGAGAAAAGAGAAACCCAGCTGCCAATCTTACG	1234
Qy	1021	TGTGTTTGGCGATGATGAGAAATGTTTCCATTGCACTGCAACCTGGAAGCA	1080
Db	1235	TGTGTTTGGCGATGATGAGAAATGTTTCCATTGCACTGCAACCTGGAAGCA	1294
Qy	1081	CATTGAAAGGCTTGCACACTGCAAGCCCTACCAAGAAAGAACAGGGGAAGCATCAAG	1140
Db	1295	CATTGAAAGGCTTGCACACTGCAAGCCCTACCAAGAAAGAACAGGGGAAGCATCAAG	1354
Qy	1141	AGTCAGAAAGCTAAGTTTAAAGAGGAGTGGCATGGCTAGCCCGGCGGCGAGTATT	1200
Db	1355	AGTCAGAAAGCTAAGTTTAAAGAGGAGTGGCATGGCTAGCCCGGCGGCGAGTATT	1414
Qy	1201	AAGAGCCGACAAAGCTCAGTAGTGAAGAGTCCCGAAGCAAGCATCAAGCCGAG	1260
Db	1415	AAGAGCCGACAAAGCTCAGTAGTGAAGAGTCCCGAAGCAAGCATCAAGCCGAG	1474
Qy	1261	GCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCTTCCGGCC	1320
Db	1475	GCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCTTCCGGCC	1534
Qy	1321	TGCTGCGGCTTCAAAAGTTTCTCAGCCAAACAGATAGATGCTGACACAGCCCTTGGC	1380
Db	1535	TGCTGCGGCTTCAAAAGTTTCTCAGCCAAACAGATAGATGCTGACACAGCCCTTGGC	1594
Qy	1381	ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGATCAGTGAAGACCTCAAC	1440
Db	1595	ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGATCAGTGAAGACCTCAAC	1654
Qy	1441	CCACCACTTAAACCTGATTCAGACTATCAGATTAATTAATTAATTCATGTTGCAACGG	1500
Db	1655	CCACCACTTAAACCTGATTCAGACTATCAGATTAATTAATTAATTCATGTTGCAACGG	1714
Qy	1501	AAGTTAAGGAAACCTTACGTCATATGATTAATTAATTAATTAATTAATTCATGTTG	1560
Db	1715	AAGTTAAGGAAACCTTACGTCATATGATTAATTAATTAATTAATTAATTCATGTTG	1774
Qy	1561	GATCATCTGACATGTTGTGATTAATTAAGCTTCAACACGCTTCAATTAATTCCT	1620
Db	1775	GATCATCTGACATGTTGTGATTAATTAAGCTTCAACACGCTTCAATTAATTCCT	1834
Qy	1621	GGAAGAGGCAATCAATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAAGCATGAG	1680
Db	1835	GGAAGAGGCAATCAATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAAGCATGAG	1894
Qy	1681	ACCAAGAGCAATCAATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAAGCATGAG	1740
Db	1895	ACCAAGAGCAATCAATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAAGCATGAG	1954
Qy	1741	ATAGAGTCAAGCTGCACTGCTACTAGACATCTAACAAGTCTCTCGAAAAGCTCT	1800
Db	1955	ATAGAGTCAAGCTGCACTGCTACTAGACATCTAACAAGTCTCTCGAAAAGCTCT	2014
Qy	1801	GCTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTAACAGCATCT	1860
Db	2015	GCTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTAACAGCATCT	2074
Qy	1861	GACTATCAAAAGCCCTGAGATGAGCAAAAGATCTTTGAGGTTCCGCAAAAGAGGCTGC	1920
Db	2075	GACTATCAAAAGCCCTGAGATGAGCAAAAGATCTTTGAGGTTCCGCAAAAGAGGCTGC	2134
Qy	1921	TTATCAGATCAACTAGTCCCAATCTCGAGAGGCTCGAGTTCAATCTGAGCGCAAT	1980
Db	2135	TTATCAGATCAACTAGTCCCAATCTCGAGAGGCTCGAGTTCAATCTGAGCGCAAT	2194
Qy	1981	GAGTTCAAGTCCAGACTTTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG	2040


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QY 1021 TGTGTTGGCGTAGTATGCGAGCTGATGAGAAACTGTGTTTCATTGCAACTTGGAGGCCA 1080
DB 1021 TGTGTTGGCGTAGTATGCGAGCTGATGAGAAACTGTGTTTCATTGCAACTTGGAGGCCA 1080
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DB 1081 CACTGGAAGGCGTTGGACACTTGCAGCCCTTACCAGAAAAACAGGGAGACATCAAGC 1140
QY 1141 AGTCAGAAAGCTAAGTTTAAAGGACGAGTGCATGGCTAGCCCCAGGGGACAGATATT 1200
DB 1116 --TCGAAAGCTAAGTTTAAAGGACGAGTGCATGGCTAGCCCCAGGGGACAGATATT 1173
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DB 1174 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTGCCCAAGACCCGATCAAGCCGAG 1233
QY 1261 GGCAGTCCGACCAAGAGTGAAGAGCTGAGCTTCAAGACCCGATCCGCTTCCGGCCC 1320
DB 1234 GGCAGTCCGACCAAGAGTGAAGAGCTGAGCTTCAAGACCCGATCCGCTTCCGGCCC 1293
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QY 1381 ACTGATGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
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QY 1561 GGTGATCTGGACATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1620
DB 1534 GGTGATCTGGACATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1593
QY 1621 GGAAGAGGCGCAATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1594 GGAAGAGGCGCAATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1653
QY 1681 ACCACAGACGATCTCAGTATGCTCGGTGCGTGGTTCAGAGTTGAAACAGGTACAGTCC 1740
DB 1654 ACCACAGACGATCTCAGTATGCTCGGTGCGTGGTTCAGAGTTGAAACAGGTACAGTCC 1713
QY 1741 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCT 1800
DB 1714 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCT 1773
QY 1801 GCGTCAGCCCTGCGCTTGGCTTCAATCCAGATCCCACTTTGAAATGTAAGACAGATCT 1860
DB 1774 GCGTCAGCCCTGCGCTTGGCTTCAATCCAGATCCCACTTTGAAATGTAAGACAGATCT 1833
QY 1861 GACTATCAAAAGCCCTGTGATGCAAAAGATCTTTGCGGTTCCGCAAAACAGTGGCTGC 1920
DB 1834 GACTATCAAAAGCCCTGTGATGCAAAAGATCTTTGCGGTTCCGCAAAACAGTGGCTGC 1893
QY 1921 TTATCCAGATCAACTAGTGCACAACTCTGAGAGGCTGCGAGTTCAATTTGAGCCCAAT 1980
DB 1894 TTATCCAGATCAACTAGTGCACAACTCTGAGAGGCTGCGAGTTCAATTTGAGCCCAAT 1953
QY 1981 GAGTTCAGTGCAGAGCTTCTACGCGGCTTAGCCCTACTATGACAGTCAAGCAACAGCAG 2040
DB 1954 GAGTTCAGTGCAGAGCTTCTACGCGGCTTAGCCCTACTATGACAGTCAAGCAACAGCAG 2013
QY 2041 GTGCCAATTATGTCAAAGCGATGGCTCAGCAGTGGAGCCACCAACCAATTGCAACCA 2100
DB 2014 GTGCCAATTATGTCAAAGCGATGGCTCAGCAGTGGAGCCACCAACCAATTGCAACCA 2073
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QY 2101 ATAAATACGGGACCCAGACAGCAGCCCAACCACTTTACAGATGCCACTTCTCTCCCA 2160
DB 2074 ATAAATACGGGACCCAGACAGCAGCCCAACCACTTTACAGATGCCACTTCTCTCCCA 2133
QY 2151 GCCATCAAGCATCTGCGCCAGGCGAGAACTCTGCAACCCCTACAGGCTTACAGAGA 2220
DB 2134 GCCATCAAGCATCTGCGCCAGGCGAGAACTCTGCAACCCCTACAGGCTTACAGAGA 2193
QY 2221 AGCATTTTGAAGTCAACCACTGCTTGTGCTTCACAGAAATGTTCAAGTTGACAG 2280
DB 2194 AGCATTTTGAAGTCAACCACTGCTTGTGCTTCACAGAAATGTTCAAGTTGACAG 2253
QY 2281 TCAATTCACCAAGGACCGTTCTATGAGAAAGCTTTGACATGAGAGAGAACTCTG 2340
DB 2254 TCAATTCACCAAGGACCGTTCTATGAGAAAGCTTTGACATGAGAGAGAACTCTG 2313
QY 2341 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
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QY 2641 AAGCAGAGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2694
DB 2614 AAGCAGAGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2667

RESULT 10
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US2002042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiele, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US2002042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT FILING DATE: US/09/825,147
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Query Match 97.4%; Score 2625.2; DB 9; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGAGTGGGCGGCGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
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106 ATGAGATGTGAGTCGGGCGGGGCGAGGTGCTGTAACCTCGGACGCGCAGGGG 165
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Db 166 GAGGGCTGTACTGCTGGGACCCGCGCGCCACGCTGTGTGGCGGCGGTGGCTTG 225
QY 121 AGGAGAGCGCGCGGGGCAAGAGGGGGCCCGGATGAGCTGTGGGGAAAGCCGCTCT 180
Db 226 AGGAGAGCGCGCGGGGCAAGAGGGGGCCCGGATGAGCTGTGGGGAAAGCCGCTCT 285
QY 181 TACACGATGACGACAGCTGCGGCGCAACGTCAAGTACCGGCGGTGCAAACTAC 240
Db 286 TACACGATGACGACAGCTGCGGCGCAACGTCAAGTACCGGCGGTGCAAACTAC 345
QY 241 TAAACGTGTGTGAGAGACCCCGCGGTGGGCGTTCATCTACACGCTTTCGTTTCTC 300
Db 346 TAAACGTGTGTGAGAGACCCCGCGGTGGGCGTTCATCTACACGCTTTCGTTTCTC 405
QY 301 CTGTGCTTGTGCTTGAATTTTGTCAAGTGTCTTCTACCATCCCTGAGCACAAATTG 360
Db 406 CTGTGCTTGTGCTTGAATTTTGTCAAGTGTCTTCTACCATCCCTGAGCACAAATTG 465
QY 361 GCGTCAAGTTGCGCTTGTGATCTGAGATTGCTGATGATGATGATGATGATGATG 420
Db 466 GCGTCAAGTTGCGCTTGTGATCTGAGATTGCTGATGATGATGATGATGATGATG 525
QY 421 ATCATTCGAAATCTGTGTCTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 526 ATCATTCGAAATCTGTGTCTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585
QY 481 AGGTTGCTCGAAGCGCTTCTGTGTATATGATACCATGTTCTTATGCTTCAATAGCA 540
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Db 706 TTCCTACATCTCTCGGACATGTGGCGCATGTGACCGAAAGGGGAGGCACTTGGAAATTA 765
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Db 826 GTTCTTATTTTTCGTCTTTCCTTGTCTATCTGTGTGAAAAGGATGCCAATAAAGATT 885
QY 781 TCTACATATGCAATGCTCTCTGTGTGGGCACAATTAATGACATATATGCTATGGA 840
Db 886 TCTACATATGCAATGCTCTCTGTGTGGGCACAATTAATGACATATATGCTATGGA 945
QY 841 GACAAAACCTCCCTAATGCTGGAGGAAATGCTTTCGACAGCTTTCGACCTTGGG 900
Db 946 GACAAAACCTCCCTAATGCTGGAGGAAATGCTTTCGACAGCTTTCGACCTTGGG 1005
QY 901 ATTTCTTTCCTTTCGACTTCCTGCGGCAATCTTGGCTCAGGTTTTCATTAAGTACA 960
Db 1006 ATTTCTTTCCTTTCGACTTCCTGCGGCAATCTTGGCTCAGGTTTTCATTAAGTACA 1065
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1186 CACTTGAAGGCTTGCACACTGACGCTTACCA----- 1220
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QY 1201 AAGAGCGCAAGAGCTCAGTAGGTGACAGAGGTGCCCAAGCAACGACATCAAGCGAG 1260
Db 1279 AAGAGCGCAAGAGCTCAGTAGGTGACAGAGGTGCCCAAGCAACGACATCAAGCGAG 1338
QY 1261 GGCAGTCCCAAGAGTGCAGAAAGAGCTGAGCTTCAACGACCGAAACCGCTTCGGGCC 1320
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Db 1399 TGCCTGCGCTCAAAAGTTCTGAGCCAAAACAGATATGATGCTGACACAGCCCTTGGC 1458
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Db 1579 AAGTTAAGAAACGTTAGCTCATATGATGTAAGATGTCATGTAACAATATCTGCT 1638
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Db 1639 GGTCACTCTGACATGTTGTGTAGAAATTAAGACCTTCAACACAGTGTGATCAAAATTC 1698
QY 1621 GGAAGAGGCAATATCATCATTAAGAAAGCCGAGAGAAATTAACAGCAAGCATGAG 1680
Db 1699 GGAAGAGGCAATATCATCATTAAGAAAGCCGAGAGAAATTAACAGCAAGCATGAG 1758
QY 1681 ACCACAGAGATCTAGATGCTCGGTGGGGGTCAAGGTTGAAGAAACAGTTACAGTCC 1740
Db 1759 ACCACAGAGATCTAGATGCTCGGTGGGGGTCAAGGTTGAAGAAACAGTTACAGTCC 1818
QY 1741 ATAGAGTCCAACTGAGTCTGCTACATGATCAACAGAGTCTTTCGAAAGGCTCT 1800
Db 1819 ATAGAGTCCAACTGAGTCTGCTACATGATCAACAGAGTCTTTCGAAAGGCTCT 1878
QY 1801 GCGTCAAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAAACAGATCT 1860
Db 1879 GCGTCAAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAAACAGATCT 1938
QY 1861 GACTATCAAGGCGCTGTGATAGCAAAAGTCTTTGGGGTTCGCAAAAAGTGGCTGC 1920
Db 1939 GACTATCAAGGCGCTGTGATAGCAAAAGTCTTTGGGGTTCGCAAAAAGTGGCTGC 1998
QY 1921 TTATCCAGATCAACTAGTGCACAACTCTCGAAGGCTGCAATTAATTCGAGCCAAAT 1980
Db 1999 TTATCCAGATCAACTAGTGCACAACTCTCGAAGGCTGCAATTAATTCGAGCCAAAT 2058
QY 1981 GAGTTCAGTGCCCAAGCTTTCAGCGGCTTACGCCCTACTGACAGTCAAGCAACAG 2040
Db 2059 GAGTTCAGTGCCCAAGCTTTCAGCGGCTTACGCCCTACTGACAGTCAAGCAACAG 2118
QY 2041 GTGCCAATTATGCAAGAGATGGCTCAGAGTGGAGCAACCAACCAATTGCAAAACCA 2100
Db 2119 GTGCCAATTATGCAAGAGATGGCTCAGAGTGGAGCAACCAACCAATTGCAAAACCA 2178
QY 2101 ATAAATACGCAACCAAGCAAGCAAGCCCAACCACTTTACAGATCCACCTCTCCCA 2160
Db 2179 ATAAATACGCAACCAAGCAAGCAAGCCCAACCACTTTACAGATCCACCTCTCCCA 2238
QY 2161 GCCATCAAGCATCTGCGCAAGGCGCAAGAACTCTGACACCTTACAGGCTTACAGGA 2220
Db 2239 GCCATCAAGCATCTGCGCAAGGCGCAAGAACTCTGACACCTTACAGGCTTACAGGA 2298
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QY 2221 AGCATTTCTGACGTCAACCACTGCTTGTGCTTCCAGAGAAATGTTGAGTTGACAG 2280
DB 2299 AGATATTTCTGACGTCAACCACTGCTTGTGCTTCCAGAGAAATGTTGAGTTGACAG 2358
QY 2281 TCMAATCTCAACCAAGACCGTTCTTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2340
DB 2359 TCMAATCTCAACCAAGACCGTTCTTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2418
QY 2341 TTGTCTGTCTGCTCCATGGTGGCGAAGGACCTTGGGCAAACTTTGCTGTGCAAAACCTG 2400
DB 2419 TTGTCTGTCTGCTCCATGGTGGCGAAGGACCTTGGGCAAACTTTGCTGTGCAAAACCTG 2478
QY 2401 ATCAGGTGACCGAGGAACTGATATATCAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2460
DB 2479 ATCAGGTGACCGAGGAACTGATATATCAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2538
QY 2461 GGCAGCCAGATTTTATACCCCAATGAGGGAATCCAAATTGTTTATTAATCTGATGAAG 2520
DB 2539 GGCAGCCAGATTTTATACCCCAATGAGGGAATCCAAATTGTTTATTAATCTGATGAAG 2598
QY 2521 GTGGGTCCGAGAGACAGAGACAGACACTTTTGTATGCGCACCGCAGCGCTGCAAGGAA 2580
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DB 2659 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGTATCTGAGACATTTGT 2718
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DB 2719 AAGGCGAGAGAAAGTACAGATGCTCCCTCAGCTTGCCTCATGTCAAACTGAATTA 2772

RESULT 11
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: Lex-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-803-268-1

Query Match 97.4%; Score 2625.2; DB 19; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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DB 106 ATGAGAGATGTGAGATCGGAGCCGAGGACAGGAGTCTGTAACCTCGGACCGCAGAGGAC 165
QY 61 GACGCGCTGTAATGCTGCTGGGACACCGCGGAGCAGGCTTGTGCGGCGCGGTGGCTTG 120

DB 166 GACGCGCTGTAATGCTGCTGGGACACCGCGGAGCAGGCTTGTGCGGCGCGGTGGCTTG 225
QY 121 AGGAGAGACCGCGGAGGAGAGAGGAGGAGCCGAGTGAAGCTGCTGAGGAGAGCGCTCT 180
DB 226 AGGAGAGACCGCGGAGGAGAGAGGAGGAGCCGAGTGAAGCTGCTGAGGAGAGCGCTCT 285
QY 181 TACAGAGTACGACAGAGCTGCGGCGCAAGTCAAGTACCGGCGGAGTCAAGTCAAGTCA 240
DB 286 TACAGAGTACGACAGAGCTGCGGCGCAAGTCAAGTACCGGCGGAGTCAAGTCAAGTCA 345
QY 241 TACAGAGTACGACAGAGCCCGCGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 300
DB 346 TACAGAGTACGACAGAGCCCGCGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 405
QY 301 CTGTCTTGTGCTGATATTTTGTCAAGTCTTCAATCCCTGAGACACAAATTTG 360
DB 406 CTGTCTTGTGCTGATATTTTGTCAAGTCTTCAATCCCTGAGACACAAATTTG 465
QY 361 GCTCAAGTGTCTTGTATCTGAGATTCGATGATTTGTGCTTTGTTGAGTTG 420
DB 466 GCTCAAGTGTCTTGTATCTGAGATTCGATGATTTGTGCTTTGTTGAGTTG 525
QY 421 ATCATTCGAATCTGTCTGCGGCTTGTGCTGATATTAAGAGATGAGAGAGAGAGCTG 480
DB 526 ATCATTCGAATCTGTCTGCGGCTTGTGCTGATATTAAGAGATGAGAGAGAGAGCTG 585
QY 481 AGGTTGCTCGAAAGCCCTTCTGCTGATATTAAGATCAATGTTGCTTATCGCTTCAATAGA 540
DB 586 AGGTTGCTCGAAAGCCCTTCTGCTGATATTAAGATCAATGTTGCTTATCGCTTCAATAGA 645
QY 541 GTTGTCTGCAAAACCTGAGGTAATATTTTGTGCAAGTCTGCAAGTCTGCAAGTCTGCA 600
DB 646 GTTGTCTGCAAAACCTGAGGTAATATTTTGTGCAAGTCTGCAAGTCTGCAAGTCTGCA 705
QY 601 TTCTCAGATCTCTCGATGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 706 TTCTCAGATCTCTCGATGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
QY 661 GGTTCAGTGTATATGCTCAGAGCAAGAGATTAATCAAGCTTGTATAGATTAAGATTTTG 720
DB 766 GGTTCAGTGTATATGCTCAGAGCAAGAGATTAATCAAGCTTGTATAGATTAAGATTTTG 825
QY 721 GTTCTTATTTTGTCTTCTTCTGCTATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 826 GTTCTTATTTTGTCTTCTTCTGCTATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 885
QY 781 TCTACATATGAGAGAGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 886 TCTACATATGAGAGAGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 945
QY 841 GACAAACCTCCCTAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 946 GACAAACCTCCCTAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
QY 901 ATTTCTTCTTGTGCACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 1006 ATTTCTTCTTGTGCACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065
QY 961 GAAACAACCGGAG 1020
DB 1066 GAAACAACCGGAG 1125
QY 1021 TGTGTTTGGCTAGTATTAAG 1080
DB 1126 TGTGTTTGGCTAGTATTAAG 1185
QY 1081 CACTTGAAGGCTTGAACCTGCAAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1186 CACTTGAAGGCTTGAACCTGCAAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1141 AGTGAAGAGCTAAGTTTAAG 1200
DB 1221 --TCAAGAGCTAAGTTTAAG 1278

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Db 345 TACACAGTAGAGCAGAGCTGCGCGCAAGTCAATGACCGGGGGGTGACAGAACTACCTG 404
QY 241 TACAAGGTCGTGAGAGAGACCCCGCGGCTGGGCTTATCTACACGCTTTCGTTTTCTC 300
Db 405 TACAAGGTCGTGAGAGAGACCCCGCGGCTGGGCTTATCTACACGCTTTCGTTTTCTC 464
QY 301 CTGTCTTTGGTGTGATGATTTTGTCTAGTGTTCCTACATCCCTGAGCACAATAATTG 360
Db 465 CTGTCTTTGGTGTGATGATTTTGTCTAGTGTTCCTACATCCCTGAGCACAATAATTG 524
QY 361 GCCTCAAGTTGCTCTTGAATCTGAGATTGAGATGATGCGTCTTTGGTTGAATTC 420
Db 525 GCCTCAAGTTGCTCTTGAATCTGAGATTGAGATGATGCGTCTTTGGTTGAATTC 584
QY 421 ATCATTCGAATCGGTGTCGCGGTTGCTGTGCTATGAGATGAGAGAGAAAGACTG 480
Db 585 ATCATTCGAATCGGTGTCGCGGTTGCTGTGCTATGAGATGAGAGAGAAAGACTG 644
QY 481 AGGTTGCTGAAAAGCCTTCTGTGTATAGATACCATGTTCTTATCGCTCAATAGCA 540
Db 645 AGGTTGCTGAAAAGCCTTCTGTGTATAGATACCATGTTCTTATCGCTCAATAGCA 704
QY 541 GTTGTCTTGCAAAAACCTCAGGGTAATATTTTGCACGCTTGCACTCAGAAATCCGT 600
Db 705 GTTGTCTTGCAAAAACCTCAGGGTAATATTTTGCACGCTTGCACTCAGAAATCCGT 764
QY 601 TTCCCTACATCTCTCGGCAATGTCGCGCATGAGACCGAAGGGAGGCACTTGAATAATCTG 660
Db 765 TTCCCTACATCTCTCGGCAATGTCGCGCATGAGACCGAAGGGAGGCACTTGAATAATCTG 824
QY 661 GGTTCAAGTGTATGCTCACAAGCAAGAAATTAATCAGACTTGTGATATAGAAATTTTG 720
Db 825 GGTTCAAGTGTATGCTCACAAGCAAGAAATTAATCAGACTTGTGATATAGAAATTTTG 884
QY 721 GTTCTTATTTTTCGTTCTTCTTCTGTCTATCTGTGTGAAAAGAGATGCCAATAAGATT 780
Db 885 GTTCTTATTTTTCGTTCTTCTTCTGTCTATCTGTGTGAAAAGAGATGCCAATAAGATT 944
QY 781 TCTACATATGAGAGTCTCTGTGTGGGGACAATTAATGACAACTATGAGCTATAGCA 840
Db 945 TCTACATATGAGAGTCTCTGTGTGGGGACAATTAATGACAACTATGAGCTATAGCA 1004
QY 841 GACAAAACCTCCCTTAATCTTGCTGGAGAAATGCTTCTGACAGGCTTTGCACTCTTGCG 900
Db 1005 GACAAAACCTCCCTTAATCTTGCTGGAGAAATGCTTCTGACAGGCTTTGCACTCTTGCG 1064
QY 901 ATTTCTTTCTTTGCACTTCTGCGCGCATTTTGGCTCAGGTTTTCATTAAAGTACA 960
Db 1065 ATTTCTTTCTTTGCACTTCTGCGCGCATTTTGGCTCAGGTTTTCATTAAAGTACA 1124
QY 961 GAAACAACACGCGCAGAAAACATTTGAGAAAAGAGAACCCAGTCCCAACTCAATTCAG 1020
Db 1125 GAAACAACACGCGCAGAAAACATTTGAGAAAAGAGAACCCAGTCCCAACTCAATTCAG 1184
QY 1021 TGTGTTTGGCTGATGATACAGCTGATGAGAAATCTGTTCCATTGCAACTTGGAAGCA 1080
Db 1185 TGTGTTTGGCTGATGATGATGAGAAATCTGTTCCATTGCAACTTGGAAGCA 1244
QY 1081 CACTTGAAAGGCTTGACACCTGACAGCCTTACCAAGAAAAGAAACAAGGGAGATCAAGC 1140
Db 1245 CACTTGAAAGGCTTGACACCTGACAGCCTTACCA----- 1279
QY 1141 AGTCGAAGACTAGTTTAAAGAGAGATGCGCATGCGTACGCGCAGGGGGCAGAGTAT 1200
Db 1280 --TCGAAGACTAGTTTAAAGAGAGATGCGCATGCGTACGCGCAGGGGGCAGAGTAT 1337
QY 1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGAGGTCCCAAGCACGACATCAACGCGAG 1260
Db 1338 AAGAGCCGACAAGCCTCAGTAGGTGACAGAGGTCCCAAGCACGACATCAACGCGAG 1397
QY 1261 GGCAGTCCCAAGAGTGAAGAGCTGAGCTTCAACGACCGAAACCGCTTCCGCGCC 1320
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Db 1398 GGCAGTCCCAAGAGTGAAGAGCTTGAGCTTCAACGACCGAACCCGCTTCCGCGCC 1457
QY 1321 TCGCGCGCCCTCAAAAGTTCTCAGCCAAACAGAGATAGATGCTGAACAGCCCTTGGC 1380
Db 1458 TCGCGCGCCCTCAAAAGTTCTCAGCCAAACAGAGATAGATGCTGAACAGCCCTTGGC 1517
QY 1381 ACTGATGATGATATGATGAAAAAGGATCCAGTGTGATGATCAGTGAAGACCTCAAC 1440
Db 1518 ACTGATGATGATATGATGAAAAAGGATCCAGTGTGATGATCAGTGAAGACCTCAAC 1577
QY 1441 CCACCACTTAAACCTGTCATTCGAGCTATCAGAAATTAAGAAATTTCAATGTCAAAACGG 1500
Db 1578 CCACCACTTAAACCTGTCATTCGAGCTATCAGAAATTAAGAAATTTCAATGTCAAAACGG 1637
QY 1501 AAGTTAAGAAAGTTACGTCATATGATGATGAAAAAGTATGATGAAATTAATTCGCT 1560
Db 1638 AAGTTAAGAAAGTTACGTCATATGATGATGAAAAAGTATGATGAAATTAATTCGCT 1697
QY 1561 GGTCACTGACATGTTGTGTAGAAATTAAGACCTTCAACACGCTGTGATCAAAATCTT 1620
Db 1698 GGTCACTGACATGTTGTGTAGAAATTAAGACCTTCAACACGCTGTGATCAAAATCTT 1757
QY 1621 GAAAAAGGGCAATCAGATCAGATAGAGAGCCGAGAGAAAATPAACAGCAACATGAG 1680
Db 1758 GAAAAAGGGCAATCAGATCAGATAGAGAGCCGAGAGAAAATPAACAGCAACATGAG 1817
QY 1681 ACCACAGACGATCTCAGATGCTCGTGGGTGGTCAAGGTTGAAAAACAGTACAGTCC 1740
Db 1818 ACCACAGACGATCTCAGATGCTCGTGGGTGGTCAAGGTTGAAAAACAGTACAGTCC 1877
QY 1741 ATAGAGTCAAGCTGAGACTGCTACTAGACATCTATCAACAGGTCCTTGGAAAAAGCTCT 1800
Db 1878 ATAGAGTCAAGCTGAGACTGCTACTAGACATCTATCAACAGGTCCTTGGAAAAAGCTCT 1937
QY 1801 GCTTCAGCCTCGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
Db 1938 GCTTCAGCCTCGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCT 1997
QY 1861 GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC 1920
Db 1998 GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC 2057
QY 1921 TTATCCAGATCAATGATGCCAAGATCTCGAGAGGCTCGAGTTCAATTCGACCGCAAT 1980
Db 2058 TTATCCAGATCAATGATGCCAAGATCTCGAGAGGCTCGAGTTCAATTCGACCGCAAT 2117
QY 1981 GAGTTCAAGTCCCAAGCTTTCTAGCGCTTACGCTTACTATGCAAGTCAACCAACAG 2040
Db 2118 GAGTTCAAGTCCCAAGCTTTCTAGCGCTTACGCTTACTATGCAAGTCAACCAACAG 2177
QY 2041 GTGCCAATTTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCCAA 2100
Db 2178 GTGCCAATTTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCCAA 2237
QY 2101 ATTAATACGAGCAACCAAGCCAGAGCCCAACAACTTTACAGATCCCACTCTCTCCA 2160
Db 2238 ATTAATACGAGCAACCAAGCCAGAGCCCAACAACTTTACAGATCCCACTCTCTCCA 2297
QY 2161 GCCATCAAGCATCTGCGCCAGAGCCAGAAAACCTGACACCTTAACCTCGACGGCTTACAGAA 2220
Db 2298 GCCATCAAGCATCTGCGCCAGAGCCAGAAAACCTGACACCTTAACCTCGACGGCTTACAGAA 2357
QY 2221 AGCATTTTCTGACGTCAACCACTGCTGTTGCTCCCAAGGAAAATGTTCAAGTTGACAG 2280
Db 2358 AGCATTTTCTGACGTCAACCACTGCTGTTGCTCCCAAGGAAAATGTTCAAGTTGACAG 2417
QY 2281 TCAATCTCAACCAAGACCGTTCTATAGAGAAAAGCTTTGACATGGAGAGAAACTCTG 2340
Db 2418 TCAATCTCAACCAAGACCGTTCTATAGGAAAAGCTTTGACATGGAGAGAAACTCTG 2477
QY 2341 TTGTCTGTCTGCTCCCATGCTGCGAGAGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2400
Db 2478 TTGTCTGTCTGCTCCCATGCTGCGAGAGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2537
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QY 2401 ATCAGGTCGACCGAGNACTGAATATATCAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2460
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Db 2538 ATAGAGTCGACCGAGAACTGAAATATACACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2597
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QY 2461 GCGAGCCAAAGATTTTATCCCAATGAGAGGAATCCAAATTTTATTAATCTGATGAAGAG 2520
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Db 2598 GCGAGCCAAAGATTTTATCCCAATGAGAGGAATCCAAATTTTATTAATCTGATGAAGAG 2657
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QY 2521 GTGGGTCCCGAAGACAGACAGACACTTTGATGCCGACCCGACCTGCGCAGAGGA 2580
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Db 2658 GTGGGTCCCGAAGACAGACAGACACTTTGATGCCGACCCGACCTGCGCAGAGGA 2717
|||
QY 2581 GCTGCTTTGCATCAGACTCTCTAAGGACTGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
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Db 2718 GCTGCTTTGCATCAGACTCTCTAAGGACTGAAGGTCAAGATCATCTCAGAGCATTTGT 2777
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QY 2641 AAGGACGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCTCAACTGAATATA 2694
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Db 2778 AAGGACGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCTCAACTGAATATA 2831
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RESULT 13
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX -0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 97.4%; Score 2625.2; DB 19; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
QY 1 ATGAAGATGTGAAGTCGGGCGGAGGAGTGTCTGTGAACTCGGACAGCGGACAGGGG 60
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Db 165 ATGAAGATGTGAAGTCGGGCGGAGGAGTGTCTGTGAACTCGGACAGCGGACAGGGG 224
|||
QY 61 GAGGCGCTGCTACTGTCTGAGGACCCGCGCGGACAGCGTGTGTGGCGGCGGTGAGCTTG 120
|||
Db 225 GAGGCGCTGCTACTGTCTGAGGACCCGCGCGGACAGCGTGTGTGGCGGCGGTGAGCTTG 284
|||
QY 121 AGGAGAGCCGCGGAGGACAGAGGGGGCCGAGATGAGCTGTGTGGGAAAGCGCTCTCT 180
|||
Db 285 AGGAGAGCCGCGGAGGACAGAGGGGGCCGAGATGAGCTGTGTGGGAAAGCGCTCTCT 344
|||
QY 181 TACAGAGTACAGAGCTGCGGCGGACAGTCAAGTACCGGGGGTGCAGACTACCTG 240
|||
Db 345 TACAGAGTACAGAGCTGCGGCGGACAGTCAAGTACCGGGGGTGCAGACTACCTG 404
|||
QY 241 TACAAGCTGTGAGAGACCCCGCGGCTGGGCTTCACTACCAAGCTTTGTTTTCTC 300
|||

Db 405 TACAAGCTGTGAGAGACCCCGCGGCTGGGCTTCACTACCAAGCTTTGTTTTCTC 464
|||
QY 301 CTGTGCTTTGTTGGCTGATTTTGTCAAGTGTCTTACCATCCCTGAGACACAAATTG 360
|||
Db 465 CTGTGCTTTGTTGGCTGATTTTGTCAAGTGTCTTACCATCCCTGAGACACAAATTG 524
|||
QY 361 GCGTCAGAGTGGCTCTGTGATCCCTGAGTGTGATGATGTGTGTGTGTGTGAGTTC 420
|||
Db 525 GCGTCAGAGTGGCTCTGTGATCCCTGAGTGTGATGATGTGTGTGTGTGTGAGTTC 584
|||
QY 421 ATCATTCGATCTGGTCTGCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
|||
Db 585 ATCATTCGATCTGGTCTGCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
|||
QY 481 AGGTTTGTGCGAAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
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Db 645 AGGTTTGTGCGAAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 704
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QY 541 GTTGTGTTTGTGCAAAAAGTCAAGGATTAATTTTGTGCGAGTCTGCACTGAGAGTCCGT 600
|||
Db 705 GTTGTGTTTGTGCAAAAAGTCAAGGATTAATTTTGTGCGAGTCTGCACTGAGAGTCCGT 764
|||
QY 601 TTCTTACAGATCTCCGCAATGAGTGGCATGACCCGAGGGAGGCACTTGGAAATTAAGT 660
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Db 765 TTCTTACAGATCTCCGCAATGAGTGGCATGACCCGAGGGAGGCACTTGGAAATTAAGT 824
|||
QY 661 GGTTCAGT 720
|||
Db 825 GGTTCAGT 884
|||
QY 721 GTTCTTAATTTTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
|||
Db 885 GTTCTTAATTTTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 944
|||
QY 781 TCTACATATGAGATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
|||
Db 945 TCTACATATGAGATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1004
|||
QY 841 GACAAAACCTCCCTTAATGT 900
|||
Db 1005 GACAAAACCTCCCTTAATGT 1064
|||
QY 901 ATTTCTTTTGTGACCTTCTCCGCAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
|||
Db 1065 ATTTCTTTTGTGACCTTCTCCGCAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1124
|||
QY 961 GAACAAACCTCCGCAAGAACCTTTGAGAAAGAGAAACCCAGCTGCCAATCTCATTCG 1020
|||
Db 1125 GAACAAACCTCCGCAAGAACCTTTGAGAAAGAGAAACCCAGCTGCCAATCTCATTCG 1184
|||
QY 1021 TGTGTTTGTGAGT 1080
|||
Db 1185 TGTGTTTGTGAGT 1244
|||
QY 1081 CACTTGAAGGCTTGTGACACTGTGAGCTTCAAGAAAGAACAGAGGAGACATCAAGC 1140
|||
Db 1245 CACTTGAAGGCTTGTGACACTGTGAGCTTCAAGAAAGAACAGAGGAGACATCAAGC 1279
|||
QY 1141 AGTCAGAACTTAAGTTTAAAGAGCGAGTGCAGTGTGATGAGCCGAGGGGCGAGATTT 1200
|||
Db 1280 --TCAAGAACTTAAGTTTAAAGAGCGAGTGCAGTGTGATGAGCCGAGGGGCGAGATTT 1337
|||
QY 1201 AAGAGCCGACAAAGCTCAATAGTGTGACAGAGAGTCCCAAGCACTGACAGCCGAG 1260
|||
Db 1338 AAGAGCCGACAAAGCTCAATAGTGTGACAGAGAGTCCCAAGCACTGACAGCCGAG 1397
|||
QY 1261 GCGAGTCCCAAGAGTGTGAGAGAGTGTGAGAGTCAAGCACTGAGAGCCGAGTTCGAGCC 1320
|||
Db 1398 GCGAGTCCCAAGAGTGTGAGAGAGTGTGAGAGTCAAGCACTGAGAGCCGAGTTCGAGCC 1457
|||
QY 1321 TCGCTGCGCTCAAAAGTTCTGAGCCAAACAGTGTATGATGTGACACAGCCCTTGGC 1380
|||
Db 1458 TCGCTGCGCTCAAAAGTTCTGAGCCAAACAGTGTATGATGTGACACAGCCCTTGGC 1517
|||

[illegible]

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OY      2461  GGCAGCCAAATTTTATCCCAATGAGGAAATCCAAATTGTTATTAACGTAGGAAG  2520
Db      2598  GCGAGCCAAATTTTATCCCAATGAGGAAATCCAAATTGTTATTAACGTAGGAAG  2657
OY      2521  GTGGTCTCCGAAGACAGACAGACACATTTTGATGCCGACCGCAGCTCCAGGAA  2580
Db      2658  GTGGTCTCCGAAGACAGACAGACACATTTTGATGCCGACCGCAGCTCCAGGAA  2717
OY      2681  GCGCCCTTTCATCAGACTCTTAAGGACGTGAAGGTCAGATCATCTCAGAGATTTGT  2640
Db      2718  GCGCCCTTTCATCAGACTCTTAAGGACGTGAAGGTCAGATCATCTCAGAGATTTGT  2777
OY      2641  AAGCAGAGAAAGTACAGATGCGCTGAGCTGCCTCATGTCAACTGAATAA  2694
Db      2778  AAGCAGAGAAAGTACAGATGCGCTGAGCTGCCTCATGTCAACTGAATAA  2831

RESULT 14
US-10-353-690-55
: Sequence 55, Application US/10353690
: Publication No. US20030215840A1
GENERAL INFORMATION:
: APPLICANT: Logan, Thomas Joseph
: APPLICANT: Chun, Miyoung
: APPLICANT: Galvin, Katherine M.
: APPLICANT: Healy, Aileen
: APPLICANT: Acton, Susan L.
: APPLICANT: Donoghue, Mary
: APPLICANT: Stegallano, Nancy
: APPLICANT: Perodrin, Jacquelin
: APPLICANT: Rodrigue-Way, Amelie
: TITLE OF INVENTION: Methods and compositions for treating
: TITLE OF INVENTION: Cardiovascular disease using 1682, 6169, 6193, 7771, 14395
: TITLE OF INVENTION: 29002, 33216, 43726, 69392, 26156, 32427, 2402, 7747, 1720
: TITLE OF INVENTION: 9151, 60451, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
: TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3464, 345, 9252, 9135,
: TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
: TITLE OF INVENTION: 283, 2254, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
: TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2250, 3474,
: FILE REFERENCE: MP102-018P1RNONAMIM
: CURRENT APPLICATION NUMBER: US/10/353,690
: CURRENT FILING DATE: 2003-01-29
: PRIOR APPLICATION NUMBER: 60/353,224
: PRIOR FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 60/354,529
: PRIOR FILING DATE: 2002-03-15
: PRIOR APPLICATION NUMBER: 60/373,861
: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: 60/376,287
: PRIOR FILING DATE: 2002-04-29
: PRIOR APPLICATION NUMBER: 60/388,080
: PRIOR FILING DATE: 2002-06-12
: PRIOR APPLICATION NUMBER: 60/390,971
: PRIOR FILING DATE: 2002-06-24
: PRIOR APPLICATION NUMBER: 60/394,130
: PRIOR FILING DATE: 2002-07-03
: PRIOR APPLICATION NUMBER: 60/394,797
: PRIOR FILING DATE: 2002-07-10
: PRIOR APPLICATION NUMBER: 60/404,904
: PRIOR FILING DATE: 2002-08-21
: PRIOR APPLICATION NUMBER: 60/405,450
: PRIOR FILING DATE: 2002-08-23
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 55
: LENGTH: 2335
: TYPE: DNA
: ORGANISM: Homo Sapiens
: US-10-353-690-55

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Best Local Similarity 60.1%; Pred. No. 2,4e-148;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

QY 217 TACCGGGGGTGCAGAACTACCTGTACAGCTGTGAGAGAGACCCGGGCTGGGCGTTG 276
Db 320 TACCGCGCGCTGCGAACTGGGTCTACACGTGTGAGGCGGCCCGCGCTGGGCGTTG 379
QY 277 ATCTACACGCTTGGTCT 336
Db 380 GTCTACACGCTCTTCAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 439
QY 337 ACCATCCCTGAGCACAACAAATTGGCTCAAGTTCCCTCTTGAATCTGAGATTGATG 396
Db 440 ACTATCAGAGAGCAGAGAACTTGGCAGAGAGTCTCTCATCTTGGAAATCGATG 499
QY 397 ATTGCTCTCTTGGTGGATTCATGATTCGAATCTGATCTGGGCTGGGCTGTTGCGA 456
Db 500 ATCTGCTTCTGGCTTGGATCATCTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 559
QY 457 TATAGAGATGAG 516
Db 560 TACCGAGATGAG 619
QY 517 ATTGTTCTTATCGCTTCAATAGAGATTGTTCTGCAAAAACGAGGTAATTTTGGCC 576
Db 620 ATCGTGTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 679
QY 577 ACCTCTGCACTAGAAAGTCTCCGTTCTCAAGATCTCCGCAATGCTGCGATGACCGA 636
Db 680 ACCTCTGCGCTGCGAGCATGCTCTCTGCAATCTCTGCGAATGCTGCGAATGACCG 739
QY 637 AGGAG 696
Db 740 CGCGGGGCGAGCTGAG 799
QY 697 ACAGCTTGTAGATAGAGATTTTGTCTTATTTTCTCTCTCTCTCTCTCTCTCTCT 756
Db 800 ACCGCTGTGATACGCGGCTTCTGCTGCTCATCTTGGCTCTCTCTCTCTCTCTCT 859
QY 757 GAAAAG 816
Db 860 GAAAAG 919
QY 817 ACATGAGAGATATGAG 876
Db 920 ACATGAGAGATATGAG 979
QY 877 TCTGAGAGCTTGGCACTCTTGGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCT 936
Db 980 GCTGCTGGCTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1039
QY 937 TCGAGTTTGGATTAAG 996
Db 1040 TCGAGTTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1099
QY 997 AACCGAG 1056
Db 1100 ATGCGGAG 1159
QY 1057 GTTTCATTTGCAACCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1107
Db 1160 GCTTACCTGAG 1219
QY 1108 CCAACCAAG 1152
Db 1220 GCCCTCTTGTGAG 1279
QY 1153 ----- 1152
Db 1280 CGCGGGGCGCGGATACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
QY 1153 -----AGTTTAAAGAGAGAG 1167

Db 1340 CGCGCGGAG 1399
QY 1168 GTGCGATGAG 1221
Db 1400 ATCCGATGAG 1459
QY 1222 GGTGAG 1278
Db 1460 ACAATCCCACTCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
QY 1279 CAG 1338
Db 1520 CAABAAG 1573
QY 1339 TCTCAG 1398
Db 1574 -----AAACCCGAG 1621
QY 1399 GAAAAG 1458
Db 1622 GAG 1681
QY 1459 ATTGAGCTATGAG 1518
Db 1682 ATCCGCTCATGAG 1741
QY 1519 CTTCTATGAG 1578
Db 1742 CGACCGTACAG 1801
QY 1579 TGTAGAGATTAAG 1635
Db 1802 GCGCGAGATAG 1861
QY 1636 ACATGAGATTAAG 1695
Db 1862 AGAAG 1921
QY 1696 AGTATGCTGAG 1755
Db 1922 ACATGATGAG 1981
QY 1756 GACTGCTATGAG 1815
Db 1982 GACTGCTATGAG 2035
QY 1816 TTGGCTTCAATTCAGATCCCACTTTTGAATGAGAGAGAGAGAGAGAGAGAGAG 1875
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QY 1876 GTGATAGCAAG 1909
Db 2096 GTGAGACCAAG 2129

RESULT 15
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US2005037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA

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? FEATURE:
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? NAME/KEY: gene
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? LOCATION: (1)..(2335)
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? LOCATION: (83)..(2170)
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US-10-850-928-1

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Matches 1103; Conservative	0;	Mismatches 566;	Indels 165;	Gaps 8;

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QY	277	ATCTACCAAGCTTTGCTTTTCTCCTGTTCTTTGGTGGCTGATTTTGTCAGTGTTTTCT	336
Db	380	GTCTACCAAGCTTTCTCATTTTTTGGTGGCTTTCAAGCTCCAGTGACTCTGTGGCTGTCC	439
QY	337	ACCAATCCCTGAGCACAAAAATTGGCCCTCAAGTGGCCCTTGATCTCTGAGATTGGTATG	396
Db	440	ACTATCCAGAGACACAGAACTTGGCCAAACGAGTCTCTCTCATTTTGGAAATTCGTATG	499
QY	397	ATTGTCGTCCTTTGTTTGGAGTTCAATTCGAATCTGATCTGGCGGTTGCTGTTGCGA	456
Db	500	ATCGTGTTTTTCGGCTTGGAGTACATCGTCGGGGTCTGGTCGGCGAGATGCTGCGCG	559
QY	457	TATAGAGATGGCAAGAAAGACTGAGTTTGCTCGAAAGCCCTTGTGTTATAGATAC	516
Db	560	TACGAGGATGGCAGGGTCTGCTTCGGCTTGGCAAAAGCCCTTGTGTCTATGCATCTTC	619
QY	517	ATTGTCCTTATCGCTTCATAGACAGTTGTTCTGCAAAAACTCAGAGGTATATTTTGGC	576
Db	620	ATCGTGTTCGTGGCCTCGGTGGCGGTCAATCGCGCGGGGTATCCAGGGCAATCTTGGCC	679
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QY	697	ACAGCTTGATCATAGAAATTTTGGTTCTATTTTTTGGTCTTCTGTCTATCTGATG	756
Db	800	ACCCCTGGTGCATCGGGTCTCTGGTGTCTATCTTGGCTCTTCTGATCACTGGCC	859
QY	757	GAAAGAATGGCAATAAAGATTTTCTACATATGAGATGCTCTGTGGTGGGGGCACATT	816
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Db	920	ACATTGCAACATATCGGCTATGATGACAAGAACCGCACATGCTGGGACGGGTCTCG	979
QY	877	TCATGAGCTTTGCACTCTTGCGCATTTTCTTCTTTCATCTTCTGCGGCATTTCTGGC	936
Db	980	GCTGCTGGCTTCGGCTTACTGCGGACATCTTTCTTTTGGCTCTGCGCGCATCTTAAGC	1039
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Db	1040	TTCGGCTTTGCTCTGAAAGTCCAGAGACGACCCGGCAGAAAGCATTTGAGAAAGCGAGG	1099
QY	997	AACCCAGCTGCAACTTCATTCAGTGTGTTTGGCGTATGTTACGACGTGATGAGAAATCT	1056
Db	1100	ATGCGCGGAGCAACCTCATCGAGGCTCCTGGCGCTGTACTCCACCGATATGAGCGG	1159
QY	1057	GTTTCCATTGGAACCTGGAAGCCACATTTGAAGGCTTGCACACTGTGACG-----	1107
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OY	1108	CCTACCAAGAAAGAAACAGGGGAAAGCATCAAGCAGTCAAGAGCTA-----	1152
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OY	1222	GGTGACAGAGGTCCTCCAGACACCGACATCAGCCGAGG---GCAGTCCACCAAGTG	1278
DB	1460	ACATATGCCACCTCTCCAGACAGACAGAGTGGGTGAGGCCACACAGCCCCACCAAGGTG	1519
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OY	1399	GAAGAAAGATGCCAGTGTGATGATCAGTGGAAAGCCTCACCCACCTTAAACTGTG	1458
DB	1622	GAGAAAGACTACCACTGTGAGCTCAGCGTGAGACATCATGCTGCTGTGAAGACAGTC	1681
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OY	1696	AGTATGTCGSGTGGGGGTCAAGGTTGAAGAAAACAGTACAGTCAATGAGTCCAAAGCTG	1755
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DB	2096	GTGGACACAGAGCATCTCCGCTCCGCAAGA	2129

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Job time : 1392.19 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 08:19:35 ; Search time 293.522 Seconds
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Title: US-09-810-796-3

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Sequence: 1 atgaagatgctgagatcgagg.....ccatgtcaactgaataa 2667

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2662.2	99.8	3111	4	US-09-825-147-3	Sequence 3, App11
3	2625.2	98.4	3137	4	US-09-590-304-1	Sequence 1, App11
4	2617.2	98.1	3074	4	US-09-813-148-1	Sequence 1, App11
5	509.8	19.1	582	4	US-09-495-050A-103	Sequence 303, App
6	492	18.4	2196	4	US-09-949-016-1823	Sequence 1823, App
7	492	18.4	2335	4	US-09-92-361-1	Sequence 1, App11
8	489.2	18.3	2273	3	US-09-177-650-88	Sequence 88, App11
9	475.6	17.8	2169	3	US-09-105-058C-22	Sequence 22, App11
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11	452	16.9	575	4	US-09-495-050A-305	Sequence 305, App
12	427.2	16.0	2565	3	US-09-105-058C-26	Sequence 26, App11
13	427.2	16.0	2914	3	US-09-177-650-6	Sequence 6, App11
14	426.8	16.0	2814	3	US-09-177-650-90	Sequence 90, App11
15	425	15.9	3287	3	US-09-105-058C-19	Sequence 19, App11
16	423.4	15.9	3232	3	US-09-177-650-1	Sequence 1, App11
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21	334.2	12.5	735	3	US-09-105-058C-7	Sequence 7, App11
22	276.4	10.4	284	4	US-09-495-050A-304	Sequence 304, App
23	267.8	10.0	2028	4	US-09-634-920-1	Sequence 1, App11
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38	266.6	10.0	2924	4	US-09-949-016-32	Sequence 32, App
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41	134.6	5.0	251	3	US-09-495-050A-296	Sequence 296, App
42	95.8	3.6	171	3	US-09-177-650-102	Sequence 102, App
43	95.8	3.6	58543	4	US-09-949-016-13565	Sequence 13565, App
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45	84.8	3.2	649	3	US-09-177-650-118	Sequence 118, App

ALIGNMENTS

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US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
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Best Local Similarity 99.9%; Pred. No. 0;
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Qy 2641 AGCTTGCTCATGTCAAACTGAATTA 2667
Db 2746 AGCTTGCTCATGTCAAACTGAATTA 2772

RESULT 2
US-09-825-147-3
Sequence 3, Application US/09825147
Patent No. 6767736
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friedlich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sandu, Arthur T.
TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
FILE REFERENCE: Lex-0160-USA
CURRENT APPLICATION NUMBER: US/09/825,147
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,255
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Paeseq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3111
TYPE: DNA
ORGANISM: homo sapiens
US-09-825-147-3

Query Match 99.8%; Score 2662.2; DB 4; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAAGATGTGAGTGGGCGGCGGCGAGGAGTGTCTGTAAGTGGAGCGGCGGCGGCG 60
Db 165 ATGAAGATGTGAGTGGGCGGCGGCGGCGAGGAGTGTCTGTAAGTGGAGCGGCGGCG 224
Qy 61 GACGGCTGCTGTAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 225 GACGGCTGCTGTAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 284
Qy 121 AGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 180
Db 285 AGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 344
Qy 181 TACAGAGTACGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
Db 345 TACAGAGTACGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 404
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Db 405 TACAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 464
Qy 301 CTGGCTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Db 465 CTGGCTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 524
Qy 361 GCCTCAAGTGGCTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
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Db 645 AGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 704
Qy 541 GTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
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Qy 661 GGTTCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 720
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Qy 841 GACAAACTCCCTTAAGTGGTGGGAGATGCTTCTGAGGCTTTCAGCTTCTTGGC 900
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Db 1065 ATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1124
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QY 2641 AGCTTGCTCATGTCAAACTGAATTA 2667
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Db 2805 AGCTTGCTCATGTCAAACTGAATTA 2831
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RESULT 3
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1
Query Match 98.4%; Score 2625.2; DB 4; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
QY 1 ATGAAGATGTGAGTGGGCGCGGCGAGGAGTGTGCTGAACTGGCAGCCGCGAGGGC 60
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Db 1 ATGAAGATGTGAGTGGGCGCGGCGAGGAGTGTGCTGAACTGGCAGCCGCGAGGGC 60
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QY 61 GACGGCTGTACTACTGTGGGCAACCGCGGCGCAAGCTTGTGTGGCGGCGGCTGGCTG 120
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DB 661 GGTTCAGTGTGTTATGCTCAACAGAAAGAAATTAAATCAACAGCTTGATCATAGAAATTTTG 720
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QY 1081 CACTTGAAGGCTTTGCAACCTGAGGCTTACCA----- 1115
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QY 1116 --TCAGAAAGCTTAAGTAAAGAGAGTGGCACTGAGTGGCCGAGGGCCAGAGTAT 1173
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QY 1234 GGCAGTCCCAAGAGTGCAGAGAGTGGAGCTTCAACGACCGACCCGCTTCCGCCC 1293
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DB 1321 TCGCTGGGCTCAAAAGTTCTCAGCCCAAAACAGTGAATGATGCTGCAAGCCCTTGGC 1380
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DB 1381 ACTGATGATGATGATGTAAGAAAGATGTCAGTGTGATGATCAGTGAAGAAGCTTACC 1440
QY 1414 CCAACCACTTAAAGCTGATTTGAGCTATCAAGAAATTAAGAAATTTTCAATTTGCAAAACG 1473
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DB 1501 AAGTTTAAGGAAAGTTAGCTCATTATGATGATGTAAGATGCTATGGAACAAATTTCTGCT 1560
QY 1534 GGTTCATCTGAGCATGTTGTGTAAGAAATTAAGGCTTCAAAACAGTGTGATCAAAATTTCT 1593
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QY 1594 GGAAGAGGCAATCAATCAATGATTAAGAAAGCCGAGAAAGAAATTAACAGCAAGAACTAG 1653
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DB 1681 ACCACAGACGATCTCAGTATGCTCGGTCCGAGTGTCAAGGTTGAAAAAGAGTACAGTCC 1740
QY 1714 ATAGAGTCCAGCTGAGTGCCTTATGACATCTATCAACAGTCTCTTGGAAAGCTCT 1773
DB 1741 ATAGAGTCCAGCTGAGTGCCTTATGACATCTATCAACAGTCTCTTGGAAAGCTCT 1800
QY 1774 GCCTCAGCCCTGCTTGGCTTCAATTCAGATCCGACCTTTGAAGTGAACGACATCT 1833
DB 1801 GCCTCAGCCCTGCTTGGCTTCAATTCAGATCCGACCTTTGAAGTGAACGACATCT 1860
QY 1834 GACTATCAAGGCTCTGATAGCAAGAAATCTTTCCGATTCGCAACAAACAGTGTCTG 1893
DB 1861 GACTATCAAGGCTCTGATAGCAAGAAATCTTTCCGATTCGCAACAAACAGTGTCTG 1920
QY 1894 TTATCCAGATCAATGATGCAACATCTGAGAGGCTTCAATTTCTGACGCCAAT 1953
DB 1921 TTATCCAGATCAATGATGCAACATCTGAGAGGCTTCAATTTCTGACGCCAAT 1980
QY 1954 GAGTTCAGTCCGAGCTTTCTTACGCGGCTTACGCGCTTATGACAGTCAAGCAACAG 2013
DB 1981 GAGTTCAGTCCGAGCTTTCTTACGCGGCTTACGCGCTTATGACAGTCAAGCAACAG 2040
QY 2014 GTGCCAATTATGATCAAAAGCATGAGTGCAGAGTGCAGCCACCAACATTCGAAACCA 2073
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QY 2134 GCCATCAAGCATGTCGCGGCGCAAGAACTGCAACCTCAACCTGCAAGCTTACAGGAA 2193
DB 2161 GCCATCAAGCATGTCGCGGCGCAAGAACTGCAACCTCAACCTGCAAGCTTACAGGAA 2220
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QY 2254 TCAATCTCAACAGGACCGTCTTATGAGAAAGCTTTGACATGAGAGAGAACTCTG 2313
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QY 2434 GGCAGCCAAAGTTTAACTCCCAATGAGAGGAATCCAAATGTTTAACTGATGAAGAG 2493
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QY 2494 GTGGGTCGCGAAGAGCAAGACACTTTTGAATGCGGACCGGAGGCTCCGAGGGA 2553
DB 2521 GTGGGTCGCGAAGAGCAAGACACTTTTGAATGCGGACCGGAGGCTCCGAGGGA 2580
QY 2554 GCTGCTTTGATCAAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2613
DB 2581 GCTGCTTTGATCAAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2640
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RESULT 4
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131


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DB 2075 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC 2134
OY 1894 TTATCCAGATCACTAGTGCACATCTCGAAGGCTGAGATTCATTCTGAGCCAAAT 1953
DB 2135 TTATCCAGATCACTAGTGCACATCTCGAAGGCTGAGATTCATTCTGAGCCAAAT 2194
OY 1954 GAGTTCAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2013
DB 2195 GAGTTCAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2254
OY 2014 GTGCCAATTAGTCAAGCGATGGCTGAGAGTGGCAAGCCCAACCAACCATTTGCAACCA 2073
DB 2255 GTGCCAATTAGTCAAGCGATGGCTGAGAGTGGCAAGCCCAACCAACCATTTGCAACCA 2314
OY 2074 ATTAATACGGACACCAAGCCAGAGCCCAACCACTTTAGATTCCTCACTCTCTCCCA 2133
DB 2315 ATTAATACGGACACCAAGCCAGAGCCCAACCACTTTAGATTCCTCACTCTCTCCCA 2374
OY 2134 GCCATCAGATCTGCCAGGCGCAAACTCTGACCCCTTACGCTGAGGCTTACAGAA 2193
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DB 2435 AGCATTTCTGACGTCACACCTGCTTGTTCCTCCAGAGAAATGTTCAAGTTGACAG 2494
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DB 2495 TCAATCTCAGCAAGACCGTTCTTATGAGAAAGCTTTGACATGGAGAGAACTCTG 2554
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OY 2494 GTGGGTCCGAGAGACAGACAGACACTTTGATGCGGCAAGGCTGCGAGAGAA 2553
DB 2735 GTGGGTCCGAGAGACAGACAGACACTTTGATGCGGCAAGGCTGCGAGAGAA 2794
OY 2554 GGTGCTTTGATCAGACTCTCTAAGAGTGAAGTCAAGATCATCTCAGACATTTGT 2613
DB 2795 GGTGCTTTGATCAGACTCTCTAAGAGTGAAGTCAAGATCATCTCAGACATTTGT 2854
OY 2614 AAGGCAAGAGAAAGTACAGATGCTTCAAGTTGCTTCAATGTAAGTGAATATA 2667
DB 2855 AAGGCAAGAGAAAGTACAGATGCTTCAAGTTGCTTCAATGTAAGTGAATATA 2908

RESULT 5
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guejler, Karl, J.
; APPLICANT: Au-Yang, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
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; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

Query Match 19.1%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 3.6e-145;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1594 GGAAGAGGCAATCATCATATAGAGAGCCGAGAGAAATACAGCAGAACTAGAG 1653
DB 1 GGAAGAGGCAATCATCATATAGAGAGCCGAGAGAAATACAGCAGAACTAGAG 60
OY 1654 ACCACAGAGATCTCAGATGCTCGGTGGGTGTTCAAGTTGAAACAGGTACAGTCC 1713
DB 61 ACCACAGAGATCTCAGATGCTCGGTGGGTGTTCAAGTTGAAACAGGTACAGTCC 120
OY 1714 ATAGAGTCCAGTGCATGCTCTTACATCTATCAACAGGTCTCTTGGAAAGCTCT 1773
DB 121 ATAGAGTCCAGTGCATGCTCTTACATCTATCAACAGGTCTCTTGGAAAGCTCT 180
OY 1774 GCCTCAGCCCTGCTTGGCTTTCATTCAGATCCACCTTTGAATGTGAAGACATCT 1833
DB 181 GCCTCAGCCCTGCTTGGCTTTCATTCAGATCCACCTTTGAATGTGAAGACATCT 240
OY 1834 GACTATCAAGCCCTGTGATAGCAAGATCTTGGGTTCCGACAAAACAGTGGCTGC 1893
DB 241 GACTATCAAGCCCTGTGATAGCAAGATCTTGGGTTCCGACAAAACAGTGGCTGC 300
OY 1894 TTATCCAGATCACTAGTGCACATCTGAGAGGCTTCAATTTGATGAGCCAAAT 1953
DB 301 TTATCCAGATCACTAGTGCACATCTGAGAGGCTTCAATTTGATGAGCCAAAT 360
OY 1954 GAGTTCAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2013
DB 361 GAGTTCAGTCCGAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 420
OY 2014 GTGCCAATTAGTCAAGCGATGGCTGAGAGTGGCAAGCCCAACCACTTTAGCAATC 2073
DB 421 GTGCCAATTAGTCAAGCGATGGCTGAGAGTGGCAAGCCCAACCACTTTAGCAATC 480
OY 2074 ATTAATACGGACACCAAGCCAGAGCCCAACCACTTTAGCAATC 2118
DB 481 ATTAATACGGACACCAAGCCAGAGCCCAACCACTTTAGCAATC 524

RESULT 6
US-09-949-016-1823
; Sequence 1823, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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: SOFTWARE: PatchQ for Windows Version 4.0
: SEQ ID NO 1823
: LENGTH: 2196
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-1823

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Query Match	18.4%	Score 492;	DB 4;	Length 2196;
Best Local Similarity	59.3%;	Pred. No. 2.7e-139;		
Matches 1087; Conservative	0;	Mismatches 555;	Indels 192;	Gaps 7,

QY	217	TACGGCGGGGTGACAAATCTACTGTACAAAGCTGTGAGAGACCCCGGGGCTGGGCGTTT	276
Db	181	TACGGCGGGCTGCAAACTGGGGGGTACAACTGCTGTGAGAGGGGCCCGGGCTGGGCGTTT	240
QY	277	ATCTACCACGCTTTCGTTTTTCTCTCTTGTCTTTGGTGTCTTGATTTTGTCAAGTGTTTCT	336
Db	241	GTCTACCAAGCTTCTCATATTTTGTGTGGTCTTCAAGCTCTGTGTGTCTGTCTGTGTCTC	300
QY	337	ACCATTCCTGTGACACAAAAATTGGCCTCAAGTTGCTCTTGTATCTTGAAGTTCGTATG	396
Db	301	ACTATCCAGAGGACACAGAACTTGGCCCAACAGATGTCTCTCATCTTGGAAATTCGTATG	360
QY	397	ATTATCGCTTTGGTTTTGGAGTTCATCATTTGAATTCGTGTGGGGTGTGCTGTGTGCA	456
Db	361	ATCTGTGTTTTGGCTTTGGAGTACATCTTCGGGGTGTGTGTGTGTGTGTGTGTGTGTG	420
QY	457	TATAGAGGATGGCAAGAAAGACTGAGTTTGCTCGAAAGCCCTTCTGTATTATAGATAC	516
Db	421	TACGAGGATGGCAGGGGTGTCTTCGCTTTGTGCAGAAAGCCCTTGTGTATGCACTTC	480
QY	517	ATTGTTCTTATCGCTTCAATAGCAAGTTGTTCTGTCAAAACTCAGGGTATATTTTGGC	576
Db	481	ATCTGTGTGTGGGCTCTGGTGGCGGTCAATCCCGGGGTATCCAGGGGCAATCTTCCGC	540
QY	577	ACGCTGTGACACAGAGTGTCCGTTTCCCTACAGATCCCGGATGTGTGCGATGGAACGA	636
Db	541	ACGTGTGGGTGTGGAGATCGCTCTCTGTGAGATCTTGGCGATGTGTGCGATGGAACGC	600
QY	637	AGGGAGGCACTTGGAAATTAATCTGGGTTACAGTGTATATGCTACAGCAAGAAATTAATC	696
Db	601	CGGGCGGCACTGTGAAGCTGTGGGCTCAATGTGTACGGGCAATGCAAGAAAGCTGATC	660
QY	697	ACAGCTTGGTACATAGAAATTTTGGTTCCTAATTTTTCGTTCCTGTCTATCTGGTG	756
Db	661	ACCGCTGTGTACATCGGGTGTCTGTGGTGTCAATCTTCGCTCTGTCTGTCTATCTGGCT	720
QY	757	GAAGAAGATGCCAATTAAGAATTTTCTACATATGAGATGTCTTGTGTGGGCGCAATTT	816
Db	721	GAGAAAGACGCCAATCGACTTCTCTCTCCATACGCCGATCGGCTCTGTGTGGGGCGAAT	780
QY	817	ACATTGACAAATATTGGCTATGAGACAAAACTCCCTTAATCTGGCTGGAGAAATTTGCTT	876
Db	781	ACATTGACAAACATCGGCTATGTGTACAGACACCGCACATATGCTTGGGCAAGGTTCTTG	840
QY	877	TCGTGACAGCTTTGCACTCTTGGCATTTCTTTCTTGTGCACTTCTGCGGCAATTTGGC	936
Db	841	GTGTGCTGGCTTCGCTTACTGTGGGATCTCTTTCTTTGTGCTGTGCGTGGGATCTTAAGC	900
QY	937	TCAGTTTGTGATTAAGTACAGAGACACACCGCCAGAAACACTTTGAAGAAAGAGG	996
Db	901	TCCGGCTTTGGCTCTGAAGGTTCAGAGAGACACCGGCGAAGACATTTGAAAGAGGGAGG	960
QY	997	AACCAGATGCCAATCTCATTCAGTGTGTGTGGGTATTTAGCAGAGCTGATGAGAAATCT	1056
Db	961	ATGCTCGGAGCAATCTCATTCAGAGCTGTCTGGGCTGTACTCTCACCGATATGAGCCGG	1020
QY	1057	GTATTCATTGCAACTGGAAAGCCAACTTGTGAAGGCTTGACACAC-----	1100
Db	1021	GCCTACTGACAGCACCTGTGTACTACTATAGACAGTATCTTCCATCTTTAGAGAGCTG	1088
QY	1101	-----	1100

Db	1081	GCCTCTTGTTAGACAGTGCAACGGGCGCCGCAATGGGAGGCTTAAGCGCCCTTGAGAGTG	1140
QY	1101	-----	1100
Db	1141	CGGCGGCGCGGTATCCCGACGAGACCTCCCGTTACCGCGCGTGTGCACCTGCGAC	1200
QY	1101	-----CTGCGAGCCCTAACCAATCAGAAAGCTTAAGTTTAAAGACGA	1140
Db	1201	CGGCGGCGGACAGACCTCCTCTCTGCTCCGTGGGGAABAGACCGGATGGGCATCAAAAGACCG	1260
QY	1141	GTGGCGCATGGCTAGCCCCAGGGGCGCAGATATT-----AAGAGCCACAAGCTTCAGTA	1194
Db	1261	ATTCGCATGGGACACTCCACGCGCGGACGGAGTCTTTCAGAGACGATCTGGACCTCCCA	1320
QY	1195	GGTGACAGGAGGTCCCGACAGCAGCATCAGACCGGAG---GCACTGCCACCAAGTG	1251
Db	1321	ACAATGCCCACTCTCCACAGCAGGACAGAGTGGTGTAGGCGACACAGCCCAACCAAGTG	1380
QY	1252	CAGAAAGCTTGAGACTTCAACGACCGAACCCTCTCCGAGCTTCGCTGCGCCTTCAAAAGT	1311
Db	1381	CAAAAGAGCTGGAGCTTCAATGACCGCACCGCTTCGGGCAATCTCGAAGACTT-----	1434
QY	1312	TCTCAGGCCAAACCAAGTATGATAGCTGACACAGCCCTTGGCACTGATGATATGAT	1371
Db	1435	-----AAACCCGCACTCTGCTGAGAGATGCC---CTTAGGGAAGTAGCAGAG	1482
QY	1372	GAAGAAAGATGCCAGTGTGATGTATCAGTGGAAAGACCTCAACCCCAACACTTAAACTGTG	1431
Db	1483	GAGAAAGACTACCACTGTGAGCTCAGCGTGAAGACATCATGCTGTGTGAAGACAGTC	1542
QY	1432	ATTGAGACTATCAGAAATTAAGAAATTTCAATGTTGCAAAACGGAAGTTTAAAGAAAGCTTA	1491
Db	1543	ATTCGCTCTCATCAGAGATTCTCAAGTTCTGTGGCCAAAAGAAATTCAGAGACACTG	1602
QY	1492	CGTCCATATGATGTAAAGATGTCAATTTGAACAAATATCTGCTGGTCACTGACATGTG	1551
Db	1603	CGACCGTACAGACGTGAAGACGTCAATTTGAGCAGTACTACAGAGGCCACCTGGACATGCTG	1662
QY	1552	TGTGAATTAAAGCCTTCAACACAGTGTGTATCAATTCTTGGAAAAGGCG---AAATC	1608
Db	1663	GCGCGGATCAAGAGCCTGCAAACTCGGGGTGAGACCAAAATTTGGGTGCGGGGCGCGGGAC	1722
QY	1609	ACATCAATTAAGAAAGACCGAGGAAATTAACAGCAACAATGAGACACAGACGATCTC	1668
Db	1723	AGGAAGCGCCGGGAGAAAGGCGACAGAGGGGCGCTCGACCGGAGGTGTGATGAATATC	1782
QY	1669	AGTATGCTCGGTGGGTGTCAAGGTGTAAAAAACAGGTACAGTCCATAGATCCAACTG	1728
Db	1783	AGCATGATGGGACGCGGTGTCAAGGTGGAAGAGAGGTGACGTCAATCGAGCAAAAGCTG	1842
QY	1729	GACTGCTTACTAGACATCTATCAACAGAGTCTTTCGAAAAGGCTCTGCTAGCCCTGCT	1788
Db	1843	GACTGCTGTGGGCTTCTATTCGCGCTGCTCG-----GCTCTGGCACTTCGGCCAGC	1896
QY	1789	TTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT	1848
Db	1897	CTGGGCGCGGTGAAGTGGCGGTGTTCGACCCCGACATCACTTCACATACAGAGCCT	1956
QY	1849	GTGATAGCAAAAGATCTTTTCGGGTTTCGCGACAAA	1882
Db	1957	GTGAGCCACGAGACATCTCGTCTCGCACAGA	1990
US-09-492-361-1 ; Sequence 1, Application US/09492361 ; Patent No. 6794161 ; GENERAL INFORMATION: ; APPLICANT: JENTSCH, Thomas J. ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE ; TITLE OF INVENTION: POTASSIUM CHANNELS ; FILE REFERENCE: 2815-127P ; CURRENT APPLICATION NUMBER: US/09/492.361			


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1 CURRENT FILING DATE: 2000-01-27
2
3 NUMBER OF SEQ ID NOS: 41
4
5 SOFTWARE: PatentIn Ver. 2.1
6
7 SEQ ID NO 1
8     LENGTH: 2335
9
10    TYPE: DNA
11
12    ORGANISM: Homo sapiens
13
14    FEATURE:
15
16        NAME/KEY: gene
17
18        LOCATION: (1)..(2335)
19
20        NAME/KEY: CDS
21
22        LOCATION: (83)..(2170)
23
24    OS-09-492-361-1

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Query Match	18.4%;	Score 492;	DB 4;	Length 2335;
Best Local Similarity	59.3%;	Pred. No. 2.9e-139;		
Matches 1087;	Conservative	0;	Mismatches 555;	Indels 192;
				Gaps 77;

Qy	217	TACGGGCGGGGAGACAACTACCTGTACAAAGCGCTGAGAGAGACC	CGCGGCGCTGGGCGTTTC	276
Db	320	TACCGCGCGCTGCAAACTGGGCTACAAACGCTGAGAGCGGCC	CCCGCGGCTGGGCGCTTC	379
Qy	277	ATCTACCAACGCTTTCGTTTTCTCCCTGTCCTTGGTCTTGATTTT	GTCACTGTTTCT	336
Db	380	GTCTACCAACGCTTCAATTTTGTGTGGCTTCACTCGCTGGTGTCT	GTCTGTGTGCTGCC	439
Qy	337	ACCATCCCTGAGCACAAAAATTTGGCCCTCAAGTTCCCTTGTATCT	TGGAGTTGGTATG	396
Db	440	ACTATCCAGAGACACAGAACTTGGCCAAACGAGTCTCTCATTTT	GGAAATTCGATATG	499
Qy	397	ATTGTCGCTTTGGTTGGTGGAGTTCATTCATTCGATCTGTGCGGG	TGTGCTGTGCGA	456
Db	500	ATCTGCTTTTCGCTTGGAGTACATGCTCGGGCTGTGCTCGCGGAT	GCCTGCTGCGCC	559
Qy	457	TATAGAGATGACAGAAAGACTGAGGTTTGCTGAAAACCTCTTGT	GTATATAGATACC	516
Db	560	TACGAGAGATGGCAGGGTTCGCTTCGCTTGGCAGAAAACCTTCT	GTGTATCATGCACTTC	619
Qy	517	ATTGTTCTTATCGCTCAATAGCAAGTTGTTCTGAAAACTCAGGGT	TAATATTTTCC	576
Db	620	ATCGTTTCGTGGCCTCGGTGGCCGTCAACGCGGGGTACCGAGG	CAACATCTTCCCC	679
Qy	577	ACGTCGCACTCAGAAAGTCTCCGTTTCTTACAGATCTCCGATGTG	CGCATGAGACGGA	636
Db	680	ACGTCCGGCTGCGGAGCATGGCTTCTGTGAGATCTCGCGATGTG	CGCATGAGACGCG	739
Qy	637	AGGAGAGGACTTGGAAATTACTGGGTTCAGTGGTTATGCTCAGAG	CAAGAAATTAATC	696
Db	740	CGCGCGGCACTTGGAACTGCTGGGCTCAGTGGTCTACGCGCATAG	CAAGAGCTGATC	799
Qy	697	ACAGCTTGTATCATAGAAATTTTGGTCTTATTTTGTCTTTCCTGT	CTCATCTGTATG	756
Db	800	ACCCCTGTGATCATCGGGTCTCTGTGTCTCATCTTCCTTCTGTAT	CACTTCCGCC	859
Qy	757	GAAAAGATGCGCAATTAAGAGTTTCTACATATGAGATGCTCTGTG	GGGACAAATTT	816
Db	860	GAGAAAGACGCAACTCCGACTTCTCTCTACGCGCATCGCTCTGT	ATGGGAGCAATTT	919
Qy	817	ACATTGACATATTTGGCTATGAGACAAAATCCCTTAATCTTGGCT	GTGGAAATTTGCTT	876
Db	920	ACATTGACAAATCTGCGCTATGTGACAAAGACACCGCACATATG	CTGTGGCGGCTCTCG	979
Qy	877	TCTGAGGCTTGTGACCTCTGGGACTTCTTCTTGTGACATTCGCG	GGGACTTCTTGGC	936
Db	980	GCTGTGCTTGTGCTTACTGGGCACTCTTCTTGTGCTGTGCGGCA	TCTTACGCC	1033
Qy	937	TCAGTTTTCATTTAAAGTACAGAACACCGCCAGAAACATTTTGA	AAAAAGAAAG	996
Db	1040	TCCGCTTTTGCCTGAAAGTCCAGAGCAGACACCGCAGAAAGCA	TTTGCAGAGAGCGAGG	1099
Qy	997	AACCCAGCTGCCAACTCATTCATGTTGTGTTGGGTAGTACGACG	CTGATGAGAAATCT	1056
Db	1100	ATGCGGAGGCAACCTCATTCAGAGCTGCTGGGCCCTGTATCTAC	CGCATATATGACCGG	1156

Qy	1057	GTTCACATTGGAACCTTGGAAGCCACACTGTAAGGCTCTTGACAC-----	1100
Dp	1160	GCCCTACCTGAGAGCCACTGTACTACTATGACATGATCCTCCATCCTTGAGAGCTG	1219
Qy	1101	-----	1100
Dp	1220	GCCTCTTGTTTGAGCAGTGCACAGGAGCCGCAATGAGGAGCTTACGAGCCCTGAGAGTG	1279
Qy	1101	-----	1100
Dp	1280	CGGCGGAGCGCCGGTACCAGCGAGCACCTCCCGTTACCOCGCCGTTGCCACTGCGAC	1339
Qy	1101	-----CTGCAGCCCTTACCAATCAGAAAGCTAAAGTTTAAAGAGCGA	1140
Dp	1340	CGGCGGGGAGCACCTCTCTTCTGCTCCCTGGGGAAGAGCGCGGATGGGATCAAGACCCG	1399
Qy	1141	GTGCGCATGTGCTAGCCCCCAAGGGGCGAGATAT-----AAGAGCGACAAAGCTCTAGTA	1194
Dp	1400	ATCCGATATGGGCAAGCTCCAGCGGCGGAGCGGGTCTTCCAAAGCAGCAGTGGCACCTCCA	1459
Qy	1195	GGTACACAGAGGTCCCCAAGCACCGACATCACAGCGAGG---GCACTCCACCAAAAGTG	1251
Dp	1460	ACAATGCCACCTCCCAAGCAGGAGACAGGTGGTATAGGCGCACAGCCACCAACAGGTG	1519
Qy	1252	CAGAAAGACTGAGACCTTCAACGACCGAACCCGCTTCGCGCCCTGCTGCGCCTCAAAAGT	1311
Dp	1520	CAAAAGAGCTGAGACTTCAATGACCGACCGCGCTTCCGGGAGATCTCTGAGACTC-----	1573
Qy	1312	TCTCAGCCAAAACGATGATAGATGCTGACACAGCCCTTGGACCTGATGATGATATGAT	1371
Dp	1574	-----AAACCCCCACCTCTGCTGAGGAGTCCC---CTTCAGAGAAAGTAGCAGAG	1621
Qy	1372	GAAAAGAGTCCAGTGTGATGATACGTGGGAAGACCTCACCCACACTTAAACGTGC	1431
Dp	1622	GAGAAAGACTACAGTGTGAGCTCACAGTGGACACATCATGCTGTGTGTAACACAGTC	1681
Qy	1432	ATTGCACTATCAGAAATTATGAATTTTCATGTTGCCAAAACGGAAGTTTAAAGAAACGTTA	1491
Dp	1682	ATCCGCTCATTACAGGATTTCTCAAGTTCTGTGGCCAAAAGGAATTTCAAGGACACTG	1741
Qy	1492	CGTCCATATGATGTAAAGAATGTCATTGAAACAATATTTCTGTGTGATCTTGACATGTTG	1551
Dp	1742	CGACCGTACGACGTGAAGGAGCAGTCAATTGAGACAGTACAGAGGCGCACCTGGACATGCTG	1801
Qy	1552	TGTGAAATTAAAGCCCTTCAAAACAGTGTGATCAAAATTCTTGGAAAAAGGCG---AAATC	1608
Dp	1802	GCGCGGATCAAGACCTGCAAACTCGGGGTGAGCCAAATGTGTGGTCCGGGAGCCCGGGAC	1861
Qy	1609	ACATCAGATTAAGAAGACCGGAGAAATAATAACAGCAGAACATGAGACACAGACGATCTC	1668
Dp	1862	AGGAAGGCCCGGGAGAAAGGGGAGCAAGGGGCGCTCGACCGGAGGAGGTGGATGAATATC	1921
Qy	1669	AGTATGCTCGGTGGGGTGTCAAGGTTGGAAAAACAGGTACAGTCAATAGACTCCAAGTGT	1728
Dp	1922	AGCATGATGGGACCGCGTGTCAAGTGTGAGAGAGCAGGTGCAATCTCATCGACCAAACTGT	1981
Qy	1729	GACGTGCTACAGACATCTATCAACAGAGTCCCTTGGAAAAGGCTGTGCTCAGCCCTGCT	1788
Dp	1982	GACCTGCTGTGGGCTTTATTTGCGCGCTGCTG-----GCTTGGCACCTCGGCGAGC	2035
Qy	1789	TTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATGTGACTATCAAGCCCT	1848
Dp	2036	CTGGGCGCCGAGCAAGTGCAGCTGTTGACCCCGACATCACTCGACTACACAGCCCT	2095
Qy	1849	GTCGATAGCAAAAGTCTTTGGGGTTCGGACAAA	1882
Dp	2096	GTCGACCAAGACATCTCCGTCTCGCACAG	2129

RESULT 8
US-09-177-650-88
; Sequence 88, Application US/09177650

Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 88
LENGTH: 2273
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(12271)
US-09-177-650-88

Query Match 18.3%; Score 489.2; DB 3; Length 2273;

Best Local Similarity 57.0%; Pred. No. 2e-138; Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;

QY 64 GGCGCTCTACTGCTGGGCAACCGCGCGGCGACGCTTGCTGGGCGCGGCTGGCGCTGAG 123
DB 67 GGGCTGTGGGCTGAGACCCCGCGCGCGCGANTCCACACGCGACGCGCNCCTACTCATC 126
QY 124 GAGAGCGCGCGGCGCAAGCAGGCGCGCGAGTAGCCTCTGGGGAAGCGCTCTCTTAC 183
DB 127 GCGGCGCTCCGAGGCGCGCGCGCGCGCANCNTTTGAGCAAGCGCGCGGCGCGCG 186
QY 184 ACGAGTAGCAGCAGAGCTCGCGCGCGCAACCTCAAGTACCGCGCGGTGAGAACTACCTGAC 243
DB 187 GGANCCGGGAAGCGCCCNANMGCAACGCGCTTCTCAACGCAAGCTGAGAAATTTCTCTAC 246
QY 244 AACGCTCTGAGAGAGACCGCGCGCGCTGGGCGCTTCTATCAAGCTTCTGTTTTCTCTT 303
DB 247 AACGCTCTGAGAGAGACCGCGCGCGCTGGGCGCTTCTATCAAGCTTCTGTTTTCTCTT 306
QY 304 GTCCTTGTGCTTGAATTTGTAGTGTCTTCTACATCTCTGAGACACAAATTTGCGC 363
DB 307 GTTCTCTCTGCGCTTGTGCTTCTGTGTTTTCCACATCAAGAGTAGAGAGACTCT 366
QY 364 TCAGATGCTCTGATCTCTGAGATTCGATGATGATGCTGCTTGTGCTTGTGAGTTCATC 423
DB 367 GAGGCGCGCGCTCTACATCTTGGAAATCGTACTATCTGCTATTCGCTTGAATCTT 426
QY 424 ATTCGATCTGATCTGCGGCTTGTGCTTGTGATATAGAGATGCGAAGAGAGACTGAG 483
DB 427 GTGAGATCTGGGCTGCGAGCTGCTGCTTCCGCTATCGAGCTGAGGCGCGAGCTCAAG 486
QY 484 TTGCTCGAAAGCGCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAAATGACATT 543
DB 487 TTGCGCAGGAAGCGCTTCTGTGATTTGATATCATGTGCTGATTCCTCAATGTGCTG 546
QY 544 GTTTCGCAAAAATCAGAGGTAATATTTTTCGACCTGCACTGAGACTGCTGCTTTC 603
DB 547 CTGGCTGCTGCTTCCAGGCAATGTCTTTCACATCTGCGTTCTGGAGCTTGGCGTTT 606
QY 604 CTACAGATCTCGCATGCTGCGCATGACCGAAGGAGAGCACTTGAATTTACTGGGT 663
DB 607 TTGCAAAATCTTGCGATGATCGTATGAGACCGAGGAGTGGCACCTGGAAGCTCTTGGGA 666
QY 664 TGAAGCTTTATGCTCAAGCAAGAAATTAATCAAGCTTGTGATCAATGAGATTTTGGTT 723
DB 667 TCGGTAGTCTAGCTCAGCAAGAGAGAGTGTGAGCTGCTGTGATCAATGTGCTTCTCTSC 726
QY 724 CTTATTTTTCGCTTTCTCTGTATCTGTGGAAGAGATGCCAATAAAGATTTTCT 783

DB 727 CTCATCTCGGCGCTCATTTCTGTGTACTTGGCAGAAAAAGGTGAGAAATGACCATTTTGAC 786
QY 784 ACATATGAGATGCTCTCGGTTGGGCAACAATTATGACAACTATTGGCTATGAGAGAC 843
DB 787 ACTTACGAGATGCTCTGTGTGGGTCTGATCACCCTGACACCAATTTGGCTACGGGAC 846
QY 844 AAAACTCCCTAACTTGGCTGGGAAGATTGCTTTTGTGAGGCTTTGCACTCTCTGGCAT 903
DB 847 AAGTACCTCAGACCTGGAGCGGAGGCTGTGGCAGCGACCTTACCTCATTTGCTGTC 906
QY 904 TCTTTCTTTGACCTTCTCGCGGCAATTTCTGGCTCAGGTTTGTGCAATTAAGTACAAGA 963
DB 907 TCGTTCTTTGCTCTTCCGCTGGCAATTTTGGATTCGGCTTTGCGCTCAAACTCAAGAG 966
QY 964 CAACCGCGCAGAAACACTTTGAGAAAAAGAAAGAACCCAGCTGCAACTCTATTGAGTGT 1023
DB 967 CAGCATCGGCAAAAACACTTTGAGAAACGGCGAACCCTGGCGCAGTCTGATCCAGTCT 1026
QY 1024 GTTGGCGTAACTTACGAGCTGAT----- 1047
DB 1027 GCTGGAATTTCTATGCTACTTAACTCTACGACCGACCTGCACTCCACGTGAGATAC 1086
QY 1048 ---GAGAAATCTGTTCCATTGCAACCTGGAAGCCACCTTGAAGCCTTGCACACCTGC 1104
DB 1087 TACGAGCGNACAGTCACTGTCCCATGTACAGCTTCAAACTCAAACTTAAGGGCTCTCC 1146
QY 1105 AGCCCTTACC-----AATCAGAAGCTTAAGTTTAA 1132
DB 1147 AGATCATCTCCACCTTGAACCAAGTGAAGCTGCTGAGAGAAATCTCAAGAGAAATCTGGA 1206
QY 1133 AGAGCGAGTGGCGATGCTGAGCCCGAGGCGCAGAGTATTAAGCCGACAGGCTCTGAG 1192
DB 1207 CTACCTTCAAGAAAGAACCCACAGCAGAGCCATCCAAAGCCCCGAGGCTGCTGCC 1266
QY 1193 TAGGTGACAGAGAGTCCCGAAGACCGACATCAAGC----- 1229
DB 1267 AAGGGAAGGGGTCTCCAGAGCCAGAGGCTCGGCGGCTCCCGAGTGGGATCAGAT 1326
QY 1230 --CGAGGCGAGTCCACCAAGAGTGCAGAGAGCTGGAAGCTTCAACGACCGGCTTTC 1287
DB 1327 CTGATGACAGCGCGAGAGAGGTGCCAAGAGCTGGAAGCTTTGTGAGCGGAGCGGACCA 1386
QY 1288 CGGCGCTGCTGCGCTTCAAAAGTTCTCAGCCAAAACAGTATGATGCTGCACAGCC 1347
DB 1387 CGCCAGGCTTTCCGATCAAGAGTCTGATCCCGCGAGAAATTCGAAAGAAAGCCCTTC 1446
QY 1348 CTGGCAGTGAATGATATATGATGAAGAAAGAGATGCCAGTGTGATATCAGTGAAGAC 1407
DB 1447 CTTGGGAGAGACATGCTAGAGACAAACAGAGCTTTAACTGCGATTTGTGACTGAAGAT 1506
QY 1408 CTCACCCACCACTTAAACCTGATTCAGCTATCAGATTTATGAAATTTCAATGTGCA 1467
DB 1507 CTTACCTCTGGGCTCAAAAGTATAGATCAGAGCGGTGTGTATGCGGTTCTTGTGATCT 1566
QY 1468 AAACGGAAGTTTAAAGAAAAGTTACGTCATATGATGTTAAAGATGTCAATTGAACAAT 1527
DB 1567 AAGCAAAAGTTCAAGAGAGTCTGGCCATATGATGTAAGAGAGTCAATCAACAGATAC 1626
QY 1528 TCTGCTGATCTGGAATGTGTGTGATTAAGACCTTCAAAACGTTGATGATCA 1587
DB 1627 TCGGCTGAGACCTTGGATATGTGTCTCCGATCAAGAGCTTGCACACAGAGTGAACG 1686
QY 1588 ATTTTGAAGAAAGGCAATATCATCAGATTAAGAGACCGAGAGAAATTAACAGAGAA 1647
DB 1687 ATTTGTGGGGCGGGGCGCAACAATAAGATTAAGAG---TCGACCAAAAGGCCCAAGGGA 1743
QY 1648 CATGAGACCAAGAGATCTCATGATGCTCGGTGGGTGTCAAGGTTGAAAAACAAGTGA 1707
DB 1744 ACGAGAGCTGCCGGAAGACCCAGAGATGAGAGCGCTTGGGAAGGTGAGAAACAGGTC 1803
QY 1708 CAGTCATAGAGTCCAGAGCTGAGCTGCTACAGCATCTATCAACAG 1755

Db	121	ATAGAAATCCAAAGCTGGAGCTGCCCTACTAACAACATCTATCAACAGGTCCTTCGGAAAGGCTCT	180
Oy	1774	GCCTCAGCCCTCGCTCTTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGACATCT	1833
Db	181	GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGACATCT	240
Oy	1834	GACATTCAAAAGCCCTGTGGATAGCAAAAGATCTTTTGGGTTCCGACAAAACAGTGGCTGC	1893
Db	241	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTGGGTTCCGACAAAACAGTGGCTGC	300
Oy	1894	TTATCCAGATCAACTAGTGCCAACTCTCGAAGGCGTCGAGTTCAATTCAGCGCAAAAT	1953
Db	301	TTATCCAGATCAACTAGTGCCAACTCTCGAAGGCGTCGAGTTCAATTCAGCGCAAAAT	359
Oy	1954	GAGTTCAGTGCCCAAGACTTCTTACCCGCGCTTAGCCCTTACTATGACACAGTCAAGCAACACAG	2013
Db	360	GAGTTCAGTGCCCAAGACTTCTTACCCGCGCTTAGCCCTTACTATGACACAGTCAAGCAACACAG	417
Oy	2014	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAAGTGGCAGCCACCAACACCATTTGCAACCCAA	2073
Db	418	GTGCCAA--TAAGTCAAAAGCGATGGCTCAGCAAGTGGCAGCCACCAACACCATTTG--AACCA	475
Oy	2074	ATTAATAAGGCAACCCAGCCAGACGCCCCCAACAACTTTCACAGATCCCACTTCCTCT	2129
Db	476	ATTATATAGGNAACCCAGCCAGACGCCCCCAACAACTTTCAGTCTCTCTCAGCTCT	531

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RESULT 12
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/ Sequence 26, Application US/09105058C
/ Patent No. 6403360
/ GENERAL INFORMATION:
/ APPLICANT: Blamar, Michael A.
/ APPLICANT: Dworetzky, Steven
/ APPLICANT: Gribkoff, Valentin K.
/ APPLICANT: Levesque, Paul C.
/ APPLICANT: Little, Wayne A.
/ APPLICANT: Neubauer, Michael G.
/ APPLICANT: Yang, Wen-Pin
/ TITLE OF INVENTION: KNO2 POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
/ FILE REFERENCE: 3053-4052
/ CURRENT APPLICATION NUMBER: US/09/105, 058C
/ CURRENT FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: US 60/055,599
/ PRIOR FILING DATE: 1997-08-12
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 2565
/ TYPE: DNA
/ ORGANISM: Homo sapiens
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QY	73	CTGCTGGGACACCGGCGGCGGACACGCTTGTTGTGGCGGGCGGGCGGATGGGCTGAGGGAGAGCGCG	132
Db	103	GTCACCTTGGCGCTTGCGGGGCGGAGCCGACAAAGCGGAGCCCTGTCTCTGAGAGGGGAGGC	162
QY	133	CGGGCGAAGCAGGGGGGCCCGGATGAGCTGTGCGGGAAAGCGCTCTTACACAGATAGC	192
Db	163	GCGCGCGACGAGGGGCGAGCGAGCACCCTCGCAGGGGCATTGGGCTCTTGAGCCAAAGCCCCG	222
QY	193	CAGAGCTGCC-----GGCGCAGCTCAAGTACCGGCGGGGTGCAGAACTACTCTGTAC	243
Db	223	CTGAGCGCCCGCAGTGCAMAGAGAAACAAGCCCAAGTACCGGCGGATCCAACCTTTGATCTAC	282

QY	244	AACGTCGTGAGAGAACCCCCGGGCGCTTACATCTAACCGCTTTCGTTTCTCTCT	303
Db	283	GACGCCCTGAGAGACCGCGGGGCGCTGGCGCTTTAACACGGGTGGTTCCTGATT	342
QY	304	GCTTTGGTGTCTGATTGTTTGTCAAGTGTTTTCTACAGTCCCTCGAGACACAAAATTGACC	363
Db	343	GTTCTGGGGGTCTTGATTCTTGCGTGTCTTGACCCATTCAAGAGATAGACTGTCTCG	402
QY	364	TCAAATTGACCTTGATCTGGAAGTTCGTATGATGATGTGCGTCTTTGGTTTGGAGTTTCATC	423
Db	403	GGAGACTGGCTTCTGTTTACTGGAGCAATTGCTATTTTTCATCTTTGGAGCCGAGTTTGGCT	462
QY	424	ATTGGAATCTGCTGCGGGTTGCTGTTTGTGATATAGAGATGGCAAGAACTGAGC	483
Db	463	TTGAGGATCTGCGGCTGCTGATGTTTGTGCTCCGATACAAAGGCTGGCGGGCCGACTGAAAG	522
QY	484	TTTGTGCGAAAGCCCTTCTGTGTTATGATATACAAATTGTCTTATTCGCTTCAATAGCAATT	543
Db	523	TTTGGCAGAAAGCCCTGTGCAATGTTGACATCTTTGTGCTGATTTGCTCTGTGCGCAATG	582
QY	544	GTTTCTGCAAAAACCTCAGGGTAAATATTTTTCGACAGTCTGCACTCAGAAAGTCCGTTTC	603
Db	583	GTGTGCTGGGAAACCAAGGCAATGTTCTGGCCACT---CCCTGCGAAGCTCGGCTTC	639
QY	604	CTACAGATCTCCGCAATGTCGCGATGAGCCGAAGGGAGGCCACTTGAAATTACTGGGT	663
Db	640	CTGCAGATCTCCGCATATGCTCGGATGAGCCGAGAGAGGTGGCACTTGAAAGCTTCTGGGC	699
QY	664	TCAGTGGTTATGCTCACAGAAAGAAATTAATCACAGTTGGTATATAGATTTTGGTT	723
Db	700	TCAGCACTGTGCCCCACAGAAAGAACTATACAGGCTGTGTAATATCGTTTCTTGACA	759
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Db	1240	CTTTCTATCTCGTGGTAGCAATACTAAAGAAAGCATTTACCTCTGAAATGTAGAT	1289
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Db	1300	GCCATAGAGAAAGTCTTTTAAAGAACCAAAAGCTGTGGCTTAAACATTAAGACGCT	1359
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; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)..(2811)

US-09-177-650-90
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Mon Oct 24 09:08:17 2005

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Page 17

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	2662.2	99.8	3111	19	US-10-803-268-3
6	2630	98.6	2694	9	US-09-866-020-1
7	2630	98.6	2694	9	US-09-810-796-2

8	2630	98.6	2694	21	US-10-948-493-1	Sequence 1, Appli
9	2625.4	98.5	3071	9	US-09-810-796-1	Sequence 1, Appli
10	2625.2	98.4	3137	19	US-10-661-629-1	Sequence 1, Appli
11	2617.2	98.1	3074	9	US-09-813-148-1	Sequence 1, Appli
12	2617.2	98.1	3074	21	US-10-399-489A-5	Sequence 5, Appli
13	2615.6	98.1	3074	21	US-10-482-834A-55	Sequence 55, Appli
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37	452	16.9	575	15	US-10-313-542-305	Sequence 10635, A
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45	427.2	16.0	2326	21	US-10-482-834A-61	Sequence 61, Appli

ALIGNMENTS

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Sequence 3, Application US/09810796
Patent No. US20020102677A1
GENERAL INFORMATION:
APPLICANT: Jega, Timothy James
TITLE OF INVENTION: KCMQ5, a No. US20020102677A1a1 Potassium Channel
FILE REFERENCE: 018512-005010US
CURRENT APPLICATION NUMBER: US/09/810,796
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/190,954
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
OTHER INFORMATION: potassium channel KCMQ5-2 coding sequence
NAME/KEY: CDS
LOCATION: (1)..(2667)
OTHER INFORMATION: KCMQ5-2
US-09-810-796-3
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Best Local Similarity 100.0%, Pred. No. 0,
Matches 2667, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 ATGAAGATGTGAGTCCGGCCCGGGCAGAGTCTGCTGAACTCCGACCCCGCAGGGC 60
DB 1 ATGAAGATGTGAGTCCGGCCCGGGCAGAGTCTGCTGAACTCCGACCCCGCAGGGC 60
QY 61 GACGGCTCTACTCTGCTGGGCAACCCGGCGGCAACGCTTGCTGGCGGGCGGTGGCTTG 120
DB 61 GACGGCTCTACTCTGCTGGGCAACCCGGCGGCAACGCTTGCTGGCGGGCGGTGGCTTG 120
QY 121 AGGAGAGCCGCGCGGGGCAAGCAGGGGGCCGGATGAGCTGCTGGGAAAGCCGCTCT 180
DB 121 AGGAGAGCCGCGCGGGGCAAGCAGGGGGCCGGATGAGCTGCTGGGAAAGCCGCTCT 180
QY 181 TACACGATGAGCCGAGCTGCGCGGCAAGTCAAGTACCGCGGGTGCAGAACTACCTG 240
DB 181 TACACGATGAGCCGAGCTGCGCGGCAAGTCAAGTACCGCGGGTGCAGAACTACCTG 240
QY 241 TACAAAGTCTGAGAGAACCCCGGGCTGGCGTTACTTACCAACGCTTTCGTTTTCTC 300
DB 241 TACAAAGTCTGAGAGAACCCCGGGCTGGCGTTACTTACCAACGCTTTCGTTTTCTC 300
QY 301 CTGTGCTTGTGCTGCTGATTTTGTCAAGTGTTCATCCATCCCTGAGCACAATAATG 360
DB 301 CTGTGCTTGTGCTGCTGATTTTGTCAAGTGTTCATCCATCCCTGAGCACAATAATG 360
QY 361 GCCTCAAGTTGCCTCTTGAATCCGAGTTCTGATGATTTGCTCTTTGGTTGAGTTT 420
DB 361 GCCTCAAGTTGCCTCTTGAATCCGAGTTCTGATGATTTGCTCTTTGGTTGAGTTT 420
QY 421 ATCATTCGAATCTGCTGCGGGTTCGTTGCTGATATAGAGATAGGCAAGAAAGACTG 480
DB 421 ATCATTCGAATCTGCTGCGGGTTCGTTGCTGATATAGAGATAGGCAAGAAAGACTG 480
QY 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTCTTACGCTTCAATAGCA 540
DB 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTCTTACGCTTCAATAGCA 540
QY 541 GTTGTTCCTGCAAAAATCAAGGGTAATTTTTTGCACGCTTGCACTGAAAGTCTCGT 600
DB 541 GTTGTTCCTGCAAAAATCAAGGGTAATTTTTTGCACGCTTGCACTGAAAGTCTCGT 600
QY 601 TTCCTACAGATCTCCTCGGAGTGGGCAAGGACCGAAGGGGAGGCACTTGGAAATTA 660
DB 601 TTCCTACAGATCTCCTCGGAGTGGGCAAGGACCGAAGGGGAGGCACTTGGAAATTA 660
QY 661 GGTTCAAGTGGTTATGCTCAAGCAAGAAATTAATCAAGCTTGGTACATAGAAATTTG 720
DB 661 GGTTCAAGTGGTTATGCTCAAGCAAGAAATTAATCAAGCTTGGTACATAGAAATTTG 720
QY 721 GTTCTTAATTTTTTCTGCTTCTTGTCTATCTGCTGAAAAGAGATCCAAATAAAGATT 780
DB 721 GTTCTTAATTTTTTCTGCTTCTTGTCTATCTGCTGAAAAGAGATCCAAATAAAGATT 780
QY 781 TCTACATATGAGATGCTCTGCTGGGGGCAAAATTAATTAACAATTAATGAGTAAGGA 840
DB 781 TCTACATATGAGATGCTCTGCTGGGGGCAAAATTAATTAACAATTAATGAGTAAGGA 840
QY 841 GACAAAACTCCCTTAATTTGCTGGGAAAGATTCTTCTGCAAGGCTTTGCACTCTTGCG 900
DB 841 GACAAAACTCCCTTAATTTGCTGGGAAAGATTCTTCTGCAAGGCTTTGCACTCTTGCG 900
QY 901 ATTTCTTTCTTTGCACTTCTGCGGCAATTTGCTGGCTCAGGTTTTCATTAAGTACAA 960
DB 901 ATTTCTTTCTTTGCACTTCTGCGGCAATTTGCTGGCTCAGGTTTTCATTAAGTACAA 960
QY 961 GAAACAACACCGCAGAAACATTTGAGAAAAGAAAGAACCCAGCTGCCAACTCAATTCG 1020
DB 961 GAAACAACACCGCAGAAACATTTGAGAAAAGAAAGAACCCAGCTGCCAACTCAATTCG 1020
QY 1021 TGTGTTTGGCGTAGTACAGCTGATGAGAAATCTGTTTCCATTGCAACCTTGAAAGCA 1080
DB 1021 TGTGTTTGGCGTAGTACAGCTGATGAGAAATCTGTTTCCATTGCAACCTTGAAAGCA 1080

QY 1081 CACTTGAAGCCCTTGACACCTTGACGCCCTTACCAATTCAGAAAGTAAAGTTTAAAGACGA 1140
DB 1081 CACTTGAAGCCCTTGACACCTTGACGCCCTTACCAATTCAGAAAGTAAAGTTTAAAGACGA 1140
QY 1141 GTGCGCAATGAGCTAAGCCCAAGGGGCGAGAGTATTAAAGCCCAAGAGCTCAGTAGTGAC 1200
DB 1141 GTGCGCAATGAGCTAAGCCCAAGGGGCGAGAGTATTAAAGCCCAAGAGCTCAGTAGTGAC 1200
QY 1201 AGAAGTCCCAAGCAGACATCAACAGCGAGGCAAGTCCACCAAGTGCAGAAAGAC 1260
DB 1201 AGAAGTCCCAAGCAGACATCAACAGCGAGGCAAGTCCACCAAGTGCAGAAAGAC 1260
QY 1261 TGGAGCTTCAACAGCCGAACCCGCTTCGGCCCTGCTGCTGCGCTCAAAAGTTCTAGCCA 1320
DB 1261 TGGAGCTTCAACAGCCGAACCCGCTTCGGCCCTGCTGCTGCGCTCAAAAGTTCTAGCCA 1320
QY 1321 AAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGAT 1380
DB 1321 AAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGAT 1380
QY 1381 TGCAGTGTGATGATCAAGTGAAGACCTCACCCCACTTAAACCTGTCATTTGAGCT 1440
DB 1381 TGCAGTGTGATGATCAAGTGAAGACCTCACCCCACTTAAACCTGTCATTTGAGCT 1440
QY 1441 ATCAGAAATTAAGAAATTTTCAATGTTGCAAAAGGAAAGTTTAAAGAAAGTTTACGTCAT 1500
DB 1441 ATCAGAAATTAAGAAATTTTCAATGTTGCAAAAGGAAAGTTTAAAGAAAGTTTACGTCAT 1500
QY 1501 GATGTAAAGATGATGATGAAATTAATTTCTGCTGCTCATCTGGAATGTTGTGAAATT 1560
DB 1501 GATGTAAAGATGATGATGAAATTAATTTCTGCTGCTCATCTGGAATGTTGTGAAATT 1560
QY 1561 AAAAGCCTTCAAAACAGTGTGATCAAAATTTCTGGAAGAAAGGCAATCAATCAGATAG 1620
DB 1561 AAAAGCCTTCAAAACAGTGTGATCAAAATTTCTGGAAGAAAGGCAATCAATCAGATAG 1620
QY 1621 AAGAGCCGAGGAAATTAACAGCAGAAATAGAGACACAGACATCTCAGATGCTCGGT 1680
DB 1621 AAGAGCCGAGGAAATTAACAGCAGAAATAGAGACACAGACATCTCAGATGCTCGGT 1680
QY 1681 CGGGTGTCAAGGTTGAAAAAACAGGTACAGTCAATAGAGTCAAGCTGAGCTGACTACTA 1740
DB 1681 CGGGTGTCAAGGTTGAAAAAACAGGTACAGTCAATAGAGTCAAGCTGAGCTGACTACTA 1740
QY 1741 GACATCTATCAACAGGCTCTTCGAAAGGCTCTGCTCAGCCCTTGCTTGGCTTCATTC 1800
DB 1741 GACATCTATCAACAGGCTCTTCGAAAGGCTCTGCTCAGCCCTTGCTTGGCTTCATTC 1800
QY 1801 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA 1860
DB 1801 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA 1860
QY 1861 GATCTTTGCGGGTTCGCGCAAAAACAGTGGCTGCTTATCAGATCAACTAGTCCAAATTC 1920
DB 1861 GATCTTTGCGGGTTCGCGCAAAAACAGTGGCTGCTTATCAGATCAACTAGTCCAAATTC 1920
QY 1921 TCGAAGGCTCTGCAAGTTCAATCTGACGCCAATGAGTTCAAGTCCCAACTTTCTAACCG 1980
DB 1921 TCGAAGGCTCTGCAAGTTCAATCTGACGCCAATGAGTTCAAGTCCCAACTTTCTAACCG 1980
QY 1981 CTAGACCTTACTATGACAGTCAAGCAACAGGTGCCAATTAATGATCAAAAGGATGAGTCA 2040
DB 1981 CTAGACCTTACTATGACAGTCAAGCAACAGGTGCCAATTAATGATCAAAAGGATGAGTCA 2040
QY 2041 GCAGTGGCAGCAACCAACCATTTGCAAAACCAATTAATTAATGAGGCAACCAAGCAGACGC 2100
DB 2041 GCAGTGGCAGCAACCAACCATTTGCAAAACCAATTAATTAATGAGGCAACCAAGCAGACGC 2100
QY 2101 CCAACCACTTTAACAGATCCGACCTCTCCCAAGCATCAAGCATCTGCGCAGGCGAAGAA 2160
DB 2101 CCAACCACTTTAACAGATCCGACCTCTCCCAAGCATCAAGCATCTGCGCAGGCGAAGAA 2160
QY 2161 ACTTGACACCCCTTAACCTTGACGGCTTACAGGAAAGCAATTTCTGACGTACACCTGCTT 2220

Db 2161 ACTCTGACACCTTAACCTGACAGGCTTAACAGAAAGCATTTCTGACGTCAACACCTGCTT 2220
Qy 2221 GTTGCTCCAGAGAAATGTTGAGTTGCACTCAAAATCTCAACAGACCGTTCTATG 2280
Db 2221 GTTGCTCCAGAGAAATGTTGAGTTGCACTCAAAATCTCAACAGACCGTTCTATG 2280
Qy 2281 AGGAAAAGCTTTGACATGAGAGAGAAACTCTGTTCTGTCTGTCTCCATGTGCGGAAG 2340
Db 2281 AGGAAAAGCTTTGACATGAGAGAGAAACTCTGTTCTGTCTGTCTCCATGTGCGGAAG 2340
Qy 2341 GACTTGGGCAATCTTTGCTGTGCAAAACCTGATCAAGTCAAGCAAGAACTGAATATA 2400
Db 2341 GACTTGGGCAATCTTTGCTGTGCAAAACCTGATCAAGTCAAGCAAGAACTGAATATA 2400
Qy 2401 CAACCTTCAAGGAGTGAATCAAGTGTCTCAAGAGCAAGCAAAATTTTAACTCCCAATAG 2460
Db 2401 CAACCTTCAAGGAGTGAATCAAGTGTCTCAAGAGCAAGCAAAATTTTAACTCCCAATAG 2460
Qy 2461 AGGGAATCCAAATGTTTATTAATCTGATGAAGAGTGGTCCGAGAGACAGAGACAGAC 2520
Db 2461 AGGGAATCCAAATGTTTATTAATCTGATGAAGAGTGGTCCGAGAGACAGAGACAGAC 2520
Qy 2521 ACTTTGATGCGCACCGACGCTGCGCAAGGAAAGTGCCTTTGCAATCAACTCTTAAG 2580
Db 2521 ACTTTGATGCGCACCGACGCTGCGCAAGGAAAGTGCCTTTGCAATCAACTCTTAAG 2580
Qy 2581 ACTGGAAGTCAAGATCAATCTCAAGACATTTGTAAGCAGAGAAAGTACAGATGCCCTC 2640
Db 2581 ACTGGAAGTCAAGATCAATCTCAAGACATTTGTAAGCAGAGAAAGTACAGATGCCCTC 2640
Qy 2641 AGCTTGCCTATGTCAAACTGAATATA 2667
Db 2641 AGCTTGCCTATGTCAAACTGAATATA 2667

RESULT 2
US-09-825-147-1
Sequence 1, Application US/09825147
Patent No. US20020042505A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: Sande, Arthur T.
FILE REFERENCE: Lex-0160-USA
CURRENT APPLICATION NUMBER: US/09/825,147
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,255
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 2772
TYPE: DNA
ORGANISM: homo sapiens
US-09-825-147-1

Query Match 99.8%; Score 2662.2; DB 9; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAAGATGTGAGTGGGCGGAGGAGGAGTGTGCTGTAATCGGACAGCGGCAAGGAG 60
Db 106 ATGAAGATGTGAGTGGGCGGAGGAGGAGTGTGCTGTAATCGGACAGCGGCAAGGAG 165
Qy 61 GACGCGCTGCTACTGCTGGGACCCGCGCGGCAAGCTTGTGGCGGCGGCTGGCCTTG 120
Db 61 GACGCGCTGCTACTGCTGGGACCCGCGCGGCAAGCTTGTGGCGGCGGCTGGCCTTG 120

Db 166 GACGCGCTGCTACTGCTGGGACCCGCGCGGCAAGCTTGTGGCGGCGGCTGGCCTTG 225
Qy 121 AGGAGAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 226 AGGAGAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
Qy 181 TACACGATGAGCAGAGTCCGCGGCAAGTCAAGTACCGGCGGAGTGAAGATCACTCTG 240
Db 286 TACACGATGAGCAGAGTCCGCGGCAAGTCAAGTACCGGCGGAGTGAAGATCACTCTG 345
Qy 241 TACACGCTGCTGAGAGAGACCCGCGGCTGGGCTTCATCTACACGCTTTCGTTTTCTC 300
Db 346 TACACGCTGCTGAGAGAGACCCGCGGCTGGGCTTCATCTACACGCTTTCGTTTTCTC 405
Qy 301 CTGTCCTTGGTGTGCTGATTTTGTGAGTGTTCATCATCCCTGAGACACAAATTTG 360
Db 406 CTGTCCTTGGTGTGCTGATTTTGTGAGTGTTCATCATCCCTGAGACACAAATTTG 465
Qy 361 GCCTCAAGTTGCTCTTGAATCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 466 GCCTCAAGTTGCTCTTGAATCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 525
Qy 421 ATCAATTCGATCTGCTGCGGCTTGTGCTGATATGAGATGAGCAGAGAGACTG 480
Db 526 ATCAATTCGATCTGCTGCGGCTTGTGCTGATATGAGATGAGCAGAGAGACTG 585
Qy 481 AGGTTTGTGAGAGCGCTTGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 586 AGGTTTGTGAGAGCGCTTGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
Qy 541 GTTGTGTTCTGCAAAAATCAGAGGATATATTTTGGCACGCTCTGCACTGAGAGTCTCCGT 600
Db 646 GTTGTGTTCTGCAAAAATCAGAGGATATATTTTGGCACGCTCTGCACTGAGAGTCTCCGT 705
Qy 601 TTCTACAGATCTCTCGCATGCTGCGCATGAGACCGAAGGAGGAGCACTTGAATTAATCTG 660
Db 706 TTCTACAGATCTCTCGCATGCTGCGCATGAGACCGAAGGAGGAGCACTTGAATTAATCTG 765
Qy 661 GGTTCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 766 GGTTCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 825
Qy 721 GTTCTTATTTTTCGCTTCTCTGCTATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 826 GTTCTTATTTTTCGCTTCTCTGCTATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 885
Qy 781 TCTACATATGAGATGCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 886 TCTACATATGAGATGCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
Qy 841 GACAAAACCTCCCTAACTTGGCTGGGAGATGCTTTCGACGAGGCTTTCACCTCCCTGGC 900
Db 946 GACAAAACCTCCCTAACTTGGCTGGGAGATGCTTTCGACGAGGCTTTCACCTCCCTGGC 1005
Qy 901 ATTTCTTCTTGGCACTTCTGCGGCAATCTTGGCTGAGGTTTTCATTTAAAGTACAA 960
Db 1006 ATTTCTTCTTGGCACTTCTGCGGCAATCTTGGCTGAGGTTTTCATTTAAAGTACAA 1065
Qy 961 GAAACAACCCGAGAAACCTTTGAGAAAGAGAAACCCGAGCTCCCACTCATTCAG 1020
Db 1066 GAAACAACCCGAGAAACCTTTGAGAAAGAGAAACCCGAGCTCCCACTCATTCAG 1125
Qy 1021 TGTGTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1126 TGTGTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1185
Qy 1081 CACTTGAAGGCTTGGACACTGACGCTTACCAATGAGAACTAAGTTTAAAGAGGCA 1140
Db 1186 CACTTGAAGGCTTGGACACTGACGCTTACCAATGAGAACTAAGTTTAAAGAGGCA 1245
Qy 1141 GTGCGATGCTAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1246 GTGCGATGCTAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1305

[illegible]

QY	2281	AGGAAAAGCTTTGACATGGGAGGAGAAACCTGTGTCTGTCTGTCCATGTGTCGGAAG	2340
Db	2286	AGGAAAAGCTTTGACATGGGAGGAGAAACCTGTGTCTGTCTGTCCATGTGTCGGAAG	2445
QY	2341	GACTTGGGCAAAATCTTGTGTGTGTGCAAAAACCTGTATCAGTGTGACCGAGAACTGAATATA	2400
Db	2446	GACTTGGGCAAAATCTTGTGTGTGTGCAAAAACCTGTATCAGTGTGACCGAGAACTGAATATA	2505
QY	2401	CAACTTTCAAGGAGTGTGTCAGTGTGCTCCAGAGGCAAGCCAAAGATTTTACCCCAATATGG	2460
Db	2506	CAACTTTCAAGGAGTGTGTCAGTGTGCTCCAGAGGCAAGCCAAAGATTTTACCCCAATATGG	2565
QY	2461	AGGGAATCCAAATTTGTTTATACATGATGAAGAGGTGGGTCCCGAAGACAGACAGACAGAC	2520
Db	2566	AGGGAATCCAAATTTGTTTATACATGATGAAGAGGTGGGTCCCGAAGACAGACAGACAGAC	2625
QY	2521	ACTTTTGATGTCGACACCGACCGACCTGTCCAGGGAAGCTTGTGCATCAGACTCTCTAAGG	2580
Db	2626	ACTTTTGATGTCGACACCGACCGACCTGTCCAGGGAAGCTTGTGCATCAGACTCTCTAAGG	2685
QY	2581	ACTGGAAAGTCACGATCATCTTCAGAGCATTTGTATAGGACAGAGAAAGTACAGATGCCCTC	2640
Db	2686	ACTGGAAAGTCACGATCATCTTCAGAGCATTTGTATAGGACAGAGAAAGTACAGATGCCCTC	2745
QY	2641	AGCTTGCTCATGTCCAAACTGAATAA	2667
Db	2746	AGCTTGCTCATGTCCAAACTGAATAA	2772

RESULT 3

US-10-803-268-1

Publication No. US20040157259A1

GENERAL INFORMATION:

APPLICANT: HU, YI

APPLICANT: Turner, C. Alexandro

APPLICANT: Nehls, Michael C.

APPLICANT: Friedrich, Glenn

APPLICANT: Zambrowicz, Brian
APPLICANT: Sands Arthur T

TITLE OF INVENTION: Novel Human

1. TITLE OF INVENTION: Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0160-USA
CIBBENT ADDICTION NUMBER: US/10/903 369

CURRENT FILING DATE: 2004-03-18

PRIOR APPLICATION NUMBER: US/09/825,147

PRIOR FILING DATE: 2001-04-03

PRIOR FILING DATE: 2000-04-03

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; NUMBER OF SEQ ID NOS: 3

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; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1
;
; LENGTH: 2772

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TYPE: DNA

ORGANISM: homo sapiens

US-10-803-268-1

Query Match 99.8%; Score 2662.2; DB 19; Length 2772

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGAAGATGTGGAGTCCGGCCGGGGCAGGGTCTGCTGAAGTCCGCAGCCCGCCAGGGGC 60

Db 106 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGCTGCTGAAGTCCGGCAGCCGGCCAGGGGC 165

61 GACGGCCTGCTACTGCTGGGCACCCCGCGCGGCCAACGCTTGGTGCGCGCGCGCGGTGCGCTG 120

Db 166 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGCGGTGGCCTG 225

121 AGGGAGAGCCGCGCGGGGCAAGCAGGGGCCCGGATGAGCCTTCTGGGGAAGCCGCTTCT 180

QY	181	TACACGATGACGACGACGCTCCGGGGGCAACGTCAGTACCCGGGGTCCAGAACTACCTG	240
Db	286	TACACGATGACGACGCTGCGGGCGCAACGTCAGTACCCGGGGTCCAGAACTACCTG	345
QY	241	TACAACTGCTGAGAGAGACCCCGCGCTGGGGCGTTCATCTACAGCTTTGCTTTTCTC	300
Db	346	TACAACTGCTGAGAGAGACCCCGGGCTGGGGCTTCATCTACAGCTTTGCTTTTCTC	405
QY	301	CTTGCTTTGGTGGTCTTGAATTTTGTCACTGTTTCTTACCATCCTGAGACACAAATTG	360
Db	406	CTTGCTTTGGTGGTCTTGAATTTTGTCACTGTTTCTTACCATCCTGAGACACAAATTG	465
QY	361	GCCTCAAGTGGCTCTTGATCCTGGAGTTCGATATTCGTCGTTGGTGGAGTTC	420
Db	466	GCCTCAAGTGGCTCTTGATCCTGGAGTTCGATATTCGTCGTTGGTGGAGTTC	525
QY	421	ATCATTCGAATCTGGTCTGCGGGTTCGTTGTTCGATATAGAGATGCAAGAACGACG	480
Db	526	ATCATTCGAATCTGGTCTGCGGGTTCGTTGTTCGATATAGAGATGCAAGAACGACG	585
QY	481	AGCTTTGCTCGAAAGCCCTTCTGTGTATAGATACATTTGTTCTTATGCTTCAATAGCA	540
Db	586	AGCTTTGCTCGAAAGCCCTTCTGTGTATAGATACATTTGTTCTTATGCTTCAATAGCA	645
QY	541	GTGTGTTCTGCAAAAACCTCAGGGTAAATTTTGTGCAAGTCGACCTCAGAAAGTCCGT	600
Db	646	GTGTGTTCTGCAAAAACCTCAGGGTAAATTTTGTGCAAGTCGACCTCAGAAAGTCCGT	705
QY	601	TTCTCTACGATCTCTCCGATGAGTGGCGCATGGAACCGAAGGGAGGCACTTGGAAATTACTG	660
Db	706	TTCTCTACGATCTCTCCGATGAGTGGCGCATGGAACCGAAGGGAGGCACTTGGAAATTACTG	765
QY	661	GGTTCAGTGGTTTATGCTCAAGCAAGGAATTTATCAAGCTTGGTATAGATTTTGTG	720
Db	766	GGTTCAGTGGTTTATGCTCAAGCAAGGAATTTATCAAGCTTGGTATAGATTTTGTG	825
QY	721	GTTCTTATTTTGGTCTCTTCTCTTCTATCTGAGTGGGAAAAAGGATGCCAATTAAGAGTTT	780
Db	826	GTTCTTATTTTGGTCTCTTCTCTTCTATCTGAGTGGGAAAAAGGATGCCAATTAAGAGTTT	885
QY	781	TCTACATATGAGATGCTCTCTGGTGGGGCAAAATTCATTTGCAACTATTTGGCTATGGA	840
Db	886	TCTACATATGAGATGCTCTCTGGTGGGGCAAAATTCATTTGCAACTATTTGGCTATGGA	945
QY	841	GACAAATCTCCCTTAACCTTGGCTGGGAAGATTGCTTTTGTGAGGCTTTGCACCTCTTGGC	900
Db	946	GACAAATCTCCCTTAACCTTGGCTGGGAAGATTGCTTTTGTGAGGCTTTGCACCTCTTGGC	1005
QY	901	ATTTCTTTCTTTGACATTCCTGCGGGCAATTCTTGGCTCAGGTTTTGCACTTAAAGTACAA	960
Db	1006	ATTTCTTTCTTTGACATTCCTGCGGGCAATTCTTGGCTCAGGTTTTGCACTTAAAGTACAA	1065
QY	961	GAAACAACCGGCCAGAAACACTTTTGAAGAAAGAGAAACCAAGCTGCCAACCTCATTCAG	1020
Db	1066	GAAACAACCGGCCAGAAACACTTTTGAAGAAAGAGAAACCAAGCTGCCAACCTCATTCAG	1125
QY	1021	TGTGTTTTGGGAGTATGATAGGAGCTGATAGAAATCTGTTTTCAATTGCAACTGTGAAGCA	1080
Db	1126	TGTGTTTTGGGAGTATGATAGGAGCTGATAGAAATCTGTTTTCAATTGCAACTGTGAAGCA	1185
QY	1081	CACCTTGAAGGCTTTGCAACCTGTGAGCCCTTACCATCAGAAAGCTTAAGTTTTAAAGAGCA	1140
Db	1186	CACCTTGAAGGCTTTGCAACCTGTGAGCCCTTACCATCAGAAAGCTTAAGTTTTAAAGAGCA	1245
QY	1141	GTGGGCATATGCTAGACCCCAAGGGGCGCAGAGTATTAAAGCCGACAAAGCTCAGTATGATAC	1200
Db	1246	GTGGGCATATGCTAGACCCCAAGGGGCGCAGAGTATTAAAGCCGACAAAGCTCAGTATGATAC	1305
QY	1201	AGGAGGTCTCCCAAGACCGGACATCAAGCCGAGGGGAGTCCCAACCAAGTSCADAAGAGC	1260
Db	1306	AGGAGGTCTCCCAAGACCGGACATCAAGCCGAGGGGAGTCCCAACCAAGTSCADAAGAGC	1365

QY	1261	TGGAGCTTCAACGACCCGACCCCGCTTCGGGCTTCGGCTCGCCCTCAAAAGTTCTCAGCA	1320
Db	1366	TGGAGCTTCAACGACCCGACCCCGCTTCGGGCTTCGGCTCGCCCTCAAAAGTTCTCAGCA	1425
QY	1331	AAACGAGTGAAGATGCTGACACAGCCCTTGCGCATGATGATATGATGAAAAAGGA	1380
Db	1426	AAACGAGTGAAGATGCTGACACAGCCCTTGCGCATGATGATATGATGAAAAAGGA	1485
QY	1381	TGCCAGTGTGATGATCAGTGAAGAAAGCCTCACCCACACTTAAACGTTCATTGAGCT	1440
Db	1486	TGCCAGTGTGATGATCAGTGAAGAAAGCCTCACCCACACTTAAACGTTCATTGAGCT	1545
QY	1441	ATCGAATATTAAGAATTTCAATGTTGCAGAAAAGGAAAGTTAAAGAAAGCTTACGTTCAT	1500
Db	1546	ATCGAATATTAAGAATTTCAATGTTGCAGAAAAGGAAAGTTAAAGAAAGCTTACGTTCAT	1605
QY	1501	GATGTAAAGATGTCATTGAAACAATTTCTGCTGATCATCTGAGCATGTTGTGATTAAT	1560
Db	1606	GATGTAAAGATGTCATTGAAACAATTTCTGCTGATCATCTGAGCATGTTGTGATTAAT	1665
QY	1561	AAAAGCCCTTCAACACGCTGTTGATCAAAATCTTGAAAAAGGCAAAATCAATCAGATAG	1620
Db	1666	AAAAGCCCTTCAACACGCTGTTGATCAAAATCTTGAAAAAGGCAAAATCAATCAGATAG	1725
QY	1621	AAGAGCCGAGAAAAATPACAGCGAAACATGAGACCCACAGCATCTTCAGTATGCTCGGT	1680
Db	1726	AAGAGCCGAGAAAAATPACAGCGAAACATGAGACCCACAGCATCTTCAGTATGCTCGGT	1785
QY	1681	CGGGTGGTCAGAGTTGAAAAACAGGTACAGTCCATAGATCCAAAGCTGAGACTGCTCTA	1740
Db	1786	CGGGTGGTCAGAGTTGAAAAACAGGTACAGTCCATAGATCCAAAGCTGAGACTGCTCTA	1845
QY	1741	GACATCTATCAACAGGTCCTTCGGAAAAAGGCTCTGAGCCCTCGCTTGGCTTCATTC	1800
Db	1846	GACATCTATCAACAGGTCCTTCGGAAAAAGGCTCTGAGCCCTCGCTTGGCTTCATTC	1905
QY	1801	CAGATCCCACTTTTGAATGTGAACAGACATCTGATCATCAAAAGCCTGTGATAGCAAA	1860
Db	1906	CAGATCCCACTTTTGAATGTGAACAGACATCTGATCATCAAAAGCCTGTGATAGCAAA	1965
QY	1861	GATCTTTCGGGTTCCGACAAAAACAGGCGCTTATCCAGATCACTAGGCCAATC	1920
Db	1966	GATCTTTCGGGTTCCGACAAAAACAGGCGCTTATCCAGATCACTAGGCCAATC	2025
QY	1921	TCGAGAGGCTCGCAGTTCATTCTGACGCCCAATAGTTCAAGTCCCGACATTTCTACGCG	1980
Db	2026	TCGAGAGGCTCGCAGTTCATTCTGACGCCCAATAGTTCAAGTCCCGACATTTCTACGCG	2085
QY	1981	CTTAGCCCTTACTATGACACGTCAAGCAACACAGGTGCCAATTAATGTCMAAGCGATGCTCA	2040
Db	2086	CTTAGCCCTTACTATGACACGTCAAGCAACACAGGTGCCAATTAATGTCMAAGCGATGCTCA	2145
QY	2041	GCAATGGCAGCACCAACACCATTTGGCAACCAATAATAACGGCACCCACAGCCAGC	2100
Db	2146	GCAATGGCAGCACCAACACCATTTGGCAACCAATAATAACGGCACCCACAGCCAGC	2205
QY	2101	CCAACAACCTTTACAGATCCCAACCTCTCCACAGCCATCAAGCATCTGCCAGGCCAGAA	2160
Db	2206	CCAACAACCTTTACAGATCCCAACCTCTCCACAGCCATCAAGCATCTGCCAGGCCAGAA	2265
QY	2161	ACTGTGACCCCTAACCCCTGACAGGCTTACAGAAAAAGATTTCTGACGTCAACACCTGCTT	2220
Db	2266	ACTGTGACCCCTAACCCCTGACAGGCTTACAGAAAAAGATTTCTGACGTCAACACCTGCTT	2325
QY	2221	GTTGCCCTTCAAGAAAAATTTTCAAGTTTGACAGTCAAAATCTCACAAAGACCGTTCTATG	2280
Db	2326	GTTGCCCTTCAAGAAAAATTTTCAAGTTTGACAGTCAAAATCTCACAAAGACCGTTCTATG	2385
QY	2281	AGAAAAAGCTTTGACATGAGAGAGAAAACTCTGTGCTCTCTGTCACCATGATGCCGAAG	2340
Db	2386	AGAAAAAGCTTTGACATGAGAGAGAAAACTCTGTGCTCTCTGTCACCATGATGCCGAAG	2445
QY	2341	GACTTGGGCAAAATCTTTGTCTGTGCAAAACCTGATCAGTCCAGAGAACTGAAATATA	2400

DB 2446 GACTTGGGAAAATCTTGTCTGTGCAAAACCTGATCAGGTGCAACGAGAACTGAATATA 2505
QY 2401 CAACCTTCAGGAGTAGTCAAGTGGCTCCAGAGGACGACCAAGATTTTACCCTAAATGG 2460
DB 2506 CAACCTTCAGGAGTAGTCAAGTGGCTCCAGAGGACGACCAAGATTTTACCCTAAATGG 2565
QY 2461 AGGGAATCCAAATTTGTTTAACTGATGAAGAAGTGGTCCGAGAGACAGAGACAGAC 2520
DB 2566 AGGGAATCCAAATTTGTTTAACTGATGAAGAAGTGGTCCGAGAGACAGAGACAGAC 2625
QY 2521 ACTTTGATGCGCGACGAGCCTGCGAGGAAAGCTGCTTGGCATCAGACTCTCTAAG 2580
DB 2626 ACTTTGATGCGCGACGAGCCTGCGAGGAAAGCTGCTTGGCATCAGACTCTCTAAG 2685
QY 2581 ACTGAAAGTCAAGCATCTCAGAGCAATTTGTAAGGACAGAAAGTACAGATGCCCTC 2640
DB 2686 ACTGAAAGTCAAGCATCTCAGAGCAATTTGTAAGGACAGAAAGTACAGATGCCCTC 2745
QY 2641 AGCTTGCTCATGTCAAACTGAATTA 2667
DB 2746 AGCTTGCTCATGTCAAACTGAATTA 2772

RESULT 4
US-09-825-147-3
Sequence 3, Application US/09825147
Patent No. US20020042505A1
GENERAL INFORMATION:
APPLICANT: Hu. Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
FILE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0160-USA
CURRENT APPLICATION NUMBER: US/09/825,147
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,255
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3111
TYPE: DNA
ORGANISM: homo sapiens
US-09-825-147-3

Query Match 99.8%; Score 2662.2; DB 9; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAAGAGATGTGAGTTCGGGCGGAGGAGGTGCTGTAACCTGGCAGCGCCAGGGGC 60
DB 165 ATGAAGAGATGTGAGTTCGGGCGGAGGAGGTGCTGTAACCTGGCAGCGCCAGGGGC 224
QY 61 GACGGCTGCTACTGCTGTGGGCAACCGGCGGCGCAGCTGTGTGGCGGGCGGTGGCCCTG 120
DB 225 GACGGCTGCTACTGCTGTGGGCAACCGGCGGCGCAGCTGTGTGGCGGGCGGTGGCCCTG 284
QY 121 AGGAGAGCGCGCGGAGCAAGAGGAGGCGCGGATGAGCTCTGTGGGAAGCGGCTCTCT 180
DB 285 AGGAGAGCGCGCGGAGCAAGAGGAGGCGCGGATGAGCTCTGTGGGAAGCGGCTCTCT 344
QY 181 TACACAGTAGTACCGAGGCTGCGGCGCAACGTCAAGTACCGGCGGCTGTGCAAACTA 240
DB 345 TACACAGTAGTACCGAGGCTGCGGCGCAACGTCAAGTACCGGCGGCTGTGCAAACTA 404
QY 241 TACACAGTAGTACCGAGGCTGCGGCGGCTGTGCAAGCTTTGCTTTTCTC 300

DB 405 TACACAGTAGTACCGAGGCTGCGGCGGCTGTGCAAGCTTTGCTTTTCTC 464
QY 301 CTGTGCTTTGGTGGTGTGATTTTGTCAAGTGTCTTACATCCCTGACACACAAATTTG 360
DB 465 CTGTGCTTTGGTGGTGTGATTTTGTCAAGTGTCTTACATCCCTGACACACAAATTTG 524
QY 361 GCCTCAAGTTGCTCTTGTATCTGTGAGTTTGTGATGATTTGTGCTTTGGTTTGAATTC 420
DB 525 GCCTCAAGTTGCTCTTGTATCTGTGAGTTTGTGATGATTTGTGCTTTGGTTTGAATTC 584
QY 421 ATCATTCGAATCTGTGCTGCGGCTGTGCTGTGATATGAGATGAGCAAGAGAGACTG 480
DB 585 ATCATTCGAATCTGTGCTGCGGCTGTGCTGTGATATGAGATGAGCAAGAGAGACTG 644
QY 481 AGGTTTGTGCAAAAGCCCTTGTGTATTAAGATACATTTGTTCTTATGCTTCAATTA 540
DB 645 AGGTTTGTGCAAAAGCCCTTGTGTATTAAGATACATTTGTTCTTATGCTTCAATTA 704
QY 541 GTTGTCTTGTCAAAATCTCAGGCTAATTTTGTGCAAGTCTGCACTCAGAACTCCGT 600
DB 705 GTTGTCTTGTCAAAATCTCAGGCTAATTTTGTGCAAGTCTGCACTCAGAACTCCGT 764
QY 601 TTCTACAGATCTTCCGATGCTGCGCATGAGACCGAAGGAGGACCTTGAATTTACTG 660
DB 765 TTCTACAGATCTTCCGATGCTGCGCATGAGACCGAAGGAGGACCTTGAATTTACTG 824
QY 661 GGTTCAGTGTATTATGCTCAGACAGGAATTAATCAAGCTTGTATAGATTTTGTG 720
DB 825 GGTTCAGTGTATTATGCTCAGACAGGAATTAATCAAGCTTGTATAGATTTTGTG 884
QY 721 GTTCTTATTTTGTGCTTCTTCTGTCTATCTGCTGTGAAAGATGCAATTAAGATTT 780
DB 885 GTTCTTATTTTGTGCTTCTTCTGTCTATCTGCTGTGAAAGATGCAATTAAGATTT 944
QY 781 TCTACATATGAGATGCTCTGCTGAGGAGCAAAATTAATTAATTAATTAATTAATTA 840
DB 945 TCTACATATGAGATGCTCTGCTGAGGAGCAAAATTAATTAATTAATTAATTAATTA 1004
QY 841 GACAAATCCCTCTAATCTTGTGAGGAATGCTTTTGTGAGGCTTGTGACTCTTGTG 900
DB 1005 GACAAATCCCTCTAATCTTGTGAGGAATGCTTTTGTGAGGCTTGTGACTCTTGTG 1064
QY 901 ATTTCTTTCTTTGCACTTCTGCGGCAATTTGCTGCTAGGTTTGTGCAATTAAGTACA 960
DB 1065 ATTTCTTTCTTTGCACTTCTGCGGCAATTTGCTGCTAGGTTTGTGCAATTAAGTACA 1124
QY 961 GAAACAACCGCGCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCAACCTCAATGAG 1020
DB 1125 GAAACAACCGCGCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCAACCTCAATGAG 1184
QY 1081 TGTGTTTGGCTGATGATGAGAGCTGATGAGAAATCTGTTTCATTTGCAACTGTGAAGCCA 1080
DB 1185 TGTGTTTGGCTGATGATGAGAGCTGATGAGAAATCTGTTTCATTTGCAACTGTGAAGCCA 1244
QY 1245 CACTTGAAGGCTTGTGCAACCTGCAAGCCTTACATGAAAGCTAAGTTTAAAGAGGA 1304
DB 1141 GTGCGCATGCTAGGCGCCAGAGGAGCAGAGTATTAAAGACCGCAAGACTCAGTAGTAGAC 1200
QY 1305 GTGCGCATGCTAGGCGCCAGAGGAGCAGAGTATTAAAGACCGCAAGACTCAGTAGTAGAC 1364
QY 1201 AGAGAGTCCCAAGACCCGATCAATCAAGCCGAGGAGCACTCCACCAAGTGCAGAGAGC 1260
DB 1365 AGAGAGTCCCAAGACCCGATCAATCAAGCCGAGGAGCACTCCACCAAGTGCAGAGAGC 1424
QY 1261 TGAAGCTTCAACGACCAACCCGCTTCCGCGCTTGTGCTGCGGCTTCAAAAGTTTCAAGCA 1320
DB 1425 TGAAGCTTCAACGACCAACCCGCTTCCGCGCTTGTGCTGCGGCTTCAAAAGTTTCAAGCA 1484
QY 1321 AAACAGTAGATAGTGTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGA 1380
DB 1485 AAACAGTAGATAGTGTGACACAGCCCTTGGCACTGATGATGATGATGAAAAAGGA 1544

QY 1381 TGGCAGTGTATGTATGATGAGAGACCTCACCCACACCTTAAAACTGTCATTGAGCT 1440
DB 1545 TGGCAGTGTATGTATGATGAGAGACCTCACCCACACCTTAAAACTGTCATTGAGCT 1604
QY 1441 ATCAAAATTAATGAAATTTTATGTTGCAAAACGAAAGTTTAAAGAAAGTTTAACTGTCAT 1500
DB 1605 ATCAAAATTAATGAAATTTTATGTTGCAAAACGAAAGTTTAAAGAAAGTTTAACTGTCAT 1664
QY 1501 GATGTAAAGATGTATGAAACAAATATTTGCTGTGTATCATGAGCACTGTGTAGAAAT 1560
DB 1665 GATGTAAAGATGTATGAAACAAATATTTGCTGTGTATCATGAGCACTGTGTAGAAAT 1724
QY 1561 AAAAGCTTCAAAACAGCTGTGTATCAATTTCTTGAAAAAGGCAAAATCACATGAGATAAG 1620
DB 1725 AAAAGCTTCAAAACAGCTGTGTATCAATTTCTTGAAAAAGGCAAAATCACATGAGATAAG 1784
QY 1621 AAGAGCCGAGAGAAATTAACAGCAAAATGAGACCAAGATCTCAAGTCTCAATGCTCGGT 1680
DB 1785 AAGAGCCGAGAGAAATTAACAGCAAAATGAGACCAAGATCTCAAGTCTCAATGCTCGGT 1844
QY 1681 CGGCTGTCAAGGTGTAAGAAACAGGTACAGTCCATAGAGTCCAAAGCTGAGCTGCTACTA 1740
DB 1845 CGGCTGTCAAGGTGTAAGAAACAGGTACAGTCCATAGAGTCCAAAGCTGAGCTGCTACTA 1904
QY 1741 GACATCTATCAACAGGTCTCTTGAAAGGCTGTGCTCAGCCCTGCTTGGCTTCAATTC 1800
DB 1905 GACATCTATCAACAGGTCTCTTGAAAGGCTGTGCTCAGCCCTGCTTGGCTTCAATTC 1964
QY 1801 CAGATCCACCTTTTGAATGTGAACAGACATCTGATCAATCAAAAGCTGTGTATAGCAA 1860
DB 1965 CAGATCCACCTTTTGAATGTGAACAGACATCTGATCAATCAAAAGCTGTGTATAGCAA 2024
QY 1861 GATCTTCCGGGTCCGACAAACAGGTGCTTATCCAGATCACTAATGTCACAAATC 1920
DB 2025 GATCTTCCGGGTCCGACAAACAGGTGCTTATCCAGATCACTAATGTCACAAATC 2084
QY 1921 TCGAGAGGCTGTGAGTTCATTTGACCCCAATAGATTAGTGCAGCCCACTTTCTACGCG 1980
DB 2085 TCGAGAGGCTGTGAGTTCATTTGACCCCAATAGATTAGTGCAGCCCACTTTCTACGCG 2144
QY 1981 CTTAGCCCTTACTATGACAGTCAAGCAACAGGTGCTCAATTTAGTCAACGATGCTCA 2040
DB 2145 CTTAGCCCTTACTATGACAGTCAAGCAACAGGTGCTCAATTTAGTCAACGATGCTCA 2204
QY 2041 GCAGTGGCAACCCCAACCAATTTGCAACCAATTAATAGCGGACCCCAAGCCAGAGCC 2100
DB 2205 GCAGTGGCAACCCCAACCAATTTGCAACCAATTAATAGCGGACCCCAAGCCAGAGCC 2264
QY 2101 CCAACAACTTTAAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
DB 2265 CCAACAACTTTAAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2324
QY 2161 ACTGTGACCCCTTAACCTGTGAGGCTTACAGAAAGCATTTTCTAGCTCAACCTGCTT 2220
DB 2325 ACTGTGACCCCTTAACCTGTGAGGCTTACAGAAAGCATTTTCTAGCTCAACCTGCTT 2284
QY 2221 GTTGGCTTCCAAAGAAATTTTCAAGTGTGACAGTCAAAATTTCAACAAAGGACCTTCTATG 2280
DB 2385 GTTGGCTTCCAAAGAAATTTTCAAGTGTGACAGTCAAAATTTCAACAAAGGACCTTCTATG 2444
QY 2281 AGGAAAAAGCTTTGACATGAGAGAGAAACTCTGTGTCTGTCTGCTCCATGAGTGCAGAG 2340
DB 2445 AGGAAAAAGCTTTGACATGAGAGAGAAACTCTGTGTCTGTCTGCTCCATGAGTGCAGAG 2504
QY 2341 GACTTGGGCAAAATCTTTGTCTGTGCAAAACCTGATCAGGTGCAACGAGAACTGAATATA 2400
DB 2505 GACTTGGGCAAAATCTTTGTCTGTGCAAAACCTGATCAGGTGCAACGAGAACTGAATATA 2564
QY 2401 CAATCTTCAAGGAGTGTGATGAGTGTCTCAAGGCGAGCCAAATTTTATCCCAAAATG 2460
DB 2565 CAATCTTCAAGGAGTGTGATGAGTGTCTCAAGGCGAGCCAAATTTTATCCCAAAATG 2624

QY 2461 AGGAAATCCAAATTTGTTTAACTGATGAAGAGTGTGTCCGAGAGAGACAGAGACAGAC 2520
DB 2625 AGGAAATCCAAATTTGTTTAACTGATGAAGAGTGTGTCCGAGAGAGACAGAGACAGAC 2684
QY 2521 ACTTTGATGCGGACACCGAGCCTGCGAGAGAAAGCTGCTTTGATCACTCAAGCTTTAAG 2580
DB 2685 ACTTTGATGCGGACACCGAGCCTGCGAGAGAAAGCTGCTTTGATCACTCAAGCTTTAAG 2744
QY 2581 ACTGAAAGGTCAAGATCATCTCAAGACATTTGTAAGGAGAGAAAGTACAGATGCCCTC 2640
DB 2745 ACTGAAAGGTCAAGATCATCTCAAGACATTTGTAAGGAGAGAAAGTACAGATGCCCTC 2804
QY 2641 AGCTTGCTCATGTCAAACTGAAATTA 2667
DB 2805 AGCTTGCTCATGTCAAACTGAAATTA 2831

RESULT 5
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 99.8%; Score 2662.2; DB 19; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAAGAGTGTGAAGTCCGGGCGGGGCAAGGTGCTGTAATCTGGCAGCCGCGAGGGGC 60
DB 165 ATGAAGAGTGTGAAGTCCGGGCGGGGCAAGGTGCTGTAATCTGGCAGCCGCGAGGGGC 224
QY 61 GACGGCTGCTACTGCTGGGCAACCGCGCGGCAAGCTTGTGTGGGCGGGGCGGCTCTG 120
DB 225 GACGGCTGCTACTGCTGGGCAACCGCGCGGCAAGCTTGTGTGGGCGGGGCGGCTCTG 284
QY 121 AGGAGAGCGCGCGGGGCAAGCAAGGGGCGCGGATGAGCTGCTGTGGGAAAGCGCTCT 180
DB 285 AGGAGAGCGCGCGGGGCAAGCAAGGGGCGCGGATGAGCTGCTGTGGGAAAGCGCTCT 344
QY 181 TACAGAGTGAAGCAGAGCTGCGGGGCAACGTCAGTACCGGCGGGGTGAGAACTAACCTG 240
DB 345 TACAGAGTGAAGCAGAGCTGCGGGGCAACGTCAGTACCGGCGGGGTGAGAACTAACCTG 404
QY 241 TACAAAGTGTGAGAGAGACCGCGCGGCTGGGCTTCACTCAACAGCTTTCGTTTTCTC 300
DB 405 TACAAAGTGTGAGAGAGACCGCGCGGCTGGGCTTCACTCAACAGCTTTCGTTTTCTC 464
QY 301 CTTGTCTTGTGTTGCTTGAATTTTGTGAGTGTCTTACCATCTGAGAGACAAATTTG 360
DB 465 CTTGTCTTGTGTTGCTTGAATTTTGTGAGTGTCTTACCATCTGAGAGACAAATTTG 524

QY	361	GCCTCAAGTTGCCCTTATCTTGAGTTCCGTGAGTTCCGTGATGATTGCTGTTGGTTGGAGTTCC	420
Db	525	GCCCTCAAGTTGCCCTTATCTTGAGTTCCGTGAGTTCCGTGAGTTCCGTGATGATTGCTGTTGGAGTTCC	584
QY	421	ATCATATGAAATCTGGTCTGCGGGTTGCTGTTGTGCAATATAGAGATGGCAAGGAAGACTG	480
Db	585	ATCATATGAAATCTGGTCTGCGGGTTGCTGTTGTGCAATATAGAGATGGCAAGGAAGACTG	644
QY	481	AGGTTTGGTGGAAAAGCCCTTCTGTGTATATAGATACCATTTGTTCTTATGCTTCAATATACA	540
Db	645	AGGTTTGGTGGAAAAGCCCTTCTGTGTATATAGATACCATTTGTTCTTATGCTTCAATATACA	704
QY	541	GTTGTTTTCGCAAAAACCTCAGGGTAATATTTTGGCAGCTGTGCACTCAGAACTCTCCGT	600
Db	705	GTTGTTTTCGCAAAAACCTCAGGGTAATATTTTGGCAGCTGTGCACTCAGAACTCTCCGT	764
QY	601	TTCCATACAGATCTCTCCGATGATGGCGCATGAGCCGAAGGGAGGCACTGGAAATTAATCTG	660
Db	765	TTCCATACAGATCTCTCCGATGATGGCGCATGAGCCGAAGGGAGGCACTGGAAATTAATCTG	824
QY	661	GGTTCAAGTGTATATGCTTCAACAGCAAGGAATTAATCAGACCTTGGTACATAGAAATTTTG	720
Db	825	GGTTCAAGTGTATATGCTTCAACAGCAAGGAATTAATCAGACCTTGGTACATAGAAATTTTG	884
QY	721	GTTCTTATATTTTGGTCTTCTTCTTCTGTCTATCTGTGGAAAAAGATGCCAATTAAGAGTTT	780
Db	885	GTTCTTATATTTTGGTCTTCTTCTTCTGTCTATCTGTGGAAAAAGATGCCAATTAAGAGTTT	944
QY	781	TCTACATATGAGATGCTCTCTGTGGGGGACAAATTAATTGACAACTATTGGCTATAGGA	840
Db	945	TCTACATATGAGATGCTCTCTGTGGGGGACAAATTAATTGACAACTATTGGCTATAGGA	1004
QY	841	GACAAAACCTCCCTTACTTGGCTGGGAAGATTGCTTTCGACAGGCTTTGCACTCTCTGGC	900
Db	1005	GACAAAACCTCCCTTACTTGGCTGGGAAGATTGCTTTCGACAGGCTTTGCACTCTCTGGC	1064
QY	901	ATTTCCTTCTTGGACCTTCGCGGGCAATCTGTGGCTCAGGTTTGGCACTTAAAGTACAA	960
Db	1065	ATTTCCTTCTTGGACCTTCGCGGGCAATCTGTGGCTCAGGTTTGGCACTTAAAGTACAA	1124
QY	961	GAAACAACCGCCGAGAAAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCTCATTCAG	1020
Db	1125	GAAACAACCGCCGAGAAAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCTCATTCAG	1184
QY	1021	TGTGTTTGGGCTAGTTACGCAAGCTGATGAGAAATCTGTTTCAATTGCAACCTGGAAGCCA	1080
Db	1185	TGTGTTTGGGCTAGTTACGCAAGCTGATGAGAAATCTGTTTCAATTGCAACCTGGAAGCCA	1244
QY	1081	CACTTGAAAGGCTTGGACACCTGCGAGCCCTCAATCAGAAAGCTBAAGTTTAAAGAGCGA	1140
Db	1245	CACTTGAAAGGCTTGGACACCTGCGAGCCCTCAATCAGAAAGCTBAAGTTTAAAGAGCGA	1304
QY	1141	GTTGGCATGTGCTAGCCCCAGGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGTGCAC	1200
Db	1305	GTTGGCATGTGCTAGCCCCAGGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGTGCAC	1364
QY	1201	AGGAGGTTCCCCAGACCTGACATTCACAGCCGAGGGCAGTCCCAACMAAGTGCAGAGAGGC	1260
Db	1365	AGGAGGTTCCCCAGACCTGACATTCACAGCCGAGGGCAGTCCCAACMAAGTGCAGAGAGGC	1424
QY	1261	TGAGAGCTTCAACGACCGAAACCCGCTTCGGGGCCCTGCGCTGCGCCCTCAAAAGTTCTCAGCA	1320
Db	1425	TGAGAGCTTCAACGACCGAAACCCGCTTCGGGGCCCTGCGCTGCGCCCTCAAAAGTTCTCAGCA	1484
QY	1321	AAACCAAGTATAGATGCTGACACAGCCCTTGGCATGATGATATGATGATGAAAGAAAGGA	1380
Db	1485	AAACCAAGTATAGATGCTGACACAGCCCTTGGCATGATGATATGATGATGAAAGAAAGGA	1544
QY	1381	TGCCAAGTGTATGATACATGATGAGGAAGACTCACCACCACTTAATAAATCTGTCAATTGAGCT	1440
Db	1545	TGCCAAGTGTATGATACATGATGAGGAAGACTCACCACCACTTAATAAATCTGTCAATTGAGCT	1604

QY	1441	ATCAGAAATTTAATGAAATTTGATGTCGAAACGGAAGCTTTAAGGAAACGTTACGTCCATAT	1500
Db	1605	ATCGAATATATGAAATTTATGTTGCAAAACGAAAGTTTAAGGAAACATATACGTCCATAT	1664
QY	1501	GATGTAATAAATATCATTTGACAAATATTTCTGCTGCTCATCTGGACATGTGTGTGAATTT	1560
Db	1665	GATGTAAATATGTCAATTTGACATATTTCTGCTGGTCACTGGACATGTGTGTGAATTT	1724
QY	1561	AAAAGCTTCAAAACAGTGTGTGATCAAAATCTTGGAAAAGGCAATCAATCAGATTAAG	1620
Db	1725	AAAAGCTTCAAAACAGTGTGTGATCAAAATCTTGGAAAAGGCAATCAATCAGATTAAG	1784
QY	1621	AAGAGCCGAGAGAAATTAACAGAGAACATGAGACACAGACGATCTCAGATATGTCGGT	1680
Db	1785	AAGAGCCGAGAGAAATTAACAGAGAACATGAGACACAGACGATCTCAGATATGTCGGT	1844
QY	1681	CGGGTGTCAAGGTTGAAAAACAGTACAGTCCATAGAGTCCAGCTGGAATGCTCTACTTA	1740
Db	1845	CGGGTGTCAAGGTTGAAAAACAGTACAGTCCATAGAGTCCAGCTGGAATGCTCTACTTA	1904
QY	1741	GACATCTATCAACAGATCCCTGCGAAAAGGCTGCTCAGCCCTGCGTTGGCTTCAATTC	1800
Db	1905	GACATCTATCAACAGATCCCTGCGAAAAGGCTGCTCAGCCCTGCGTTGGCTTCAATTC	1964
QY	1801	CAGATCCCACTTTTAAATGATGTAACAGACATCTGACTATCAAAAGCCCTGCGATTAACAA	1860
Db	1965	CAGATCCCACTTTTAAATGATGTAACAGACATCTGACTATCAAAAGCCCTGCGATTAACAA	2024
QY	1861	GATCTTTCCGGGTCCCGCACAAAACAGTGGCTCTTATCAAGATCAACTATGTCGAACATC	1920
Db	2025	GATCTTTCCGGGTCCCGCACAAAACAGTGGCTCTTATCAAGATCAACTATGTCGAACATC	2084
QY	1921	TCGAGAGGCTGTGAGTTCATTCATGACGCCAAATGAGTTCAAGTCCCAACTTTCTACGCG	1980
Db	2085	TCGAGAGGCTGTGAGTTCATTCATGACGCCAAATGAGTTCAAGTCCCAACTTTCTACGCG	2144
QY	1981	CTTAGCCCTATCTATGTCACAGTCAGCAACACAGGTGCCAATTAATGTCAAAGCGATGCTCA	2040
Db	2145	CTTAGCCCTACTATGTCACAGTCAGCAACACAGGTGCCAATTAATGTCAAAGCGATGCTCA	2204
QY	2041	GCAGTGGACGCCCAACAACCAATTGGAAACCAATTAATAAGGACCCGACAGCGACAGCGC	2100
Db	2205	GCAGTGGACGCCCAACAACCAATTGGAAACCAATTAATAAGGACCCGACAGCGACAGCGC	2264
QY	2101	CCAACAACCTTTACAGATCCCACTCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA	2160
Db	2265	CCAACAACCTTTACAGATCCCACTCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA	2324
QY	2161	ACCTGTCACCCCTAACCCCTGACGGCTTACAGAAACATTTCTGACGTACCAACCTGCTT	2220
Db	2325	ACCTGTCACCCCTAACCCCTGACGGCTTACAGAAACATTTCTGACGTACCAACCTGCTT	2384
QY	2221	GTTGACCTCAAGGAAATATTTGAGGTGACAGTCAAAATCTCACCAAGAACCGTTCATATG	2280
Db	2385	GTTGACCTCAAGGAAATATTTGAGGTGACAGTCAAAATCTCACCAAGAACCGTTCATATG	2444
QY	2281	AGGAAAAAGCTTTGACATGCGAGAGAGAAATCTGTGTTCTGTCTGTCCATGTGCGAAG	2340
Db	2445	AGGAAAAAGCTTTGACATGCGAGAGAGAAATCTGTGTTCTGTCTGTCCATGTGCGAAG	2504
QY	2341	GACCTGGGCAAAATCTTTGTCGTGCAAAACCTGATCAGGTGGAACCGAGAACTGAAATTA	2400
Db	2505	GACCTGGGCAAAATCTTTGTCGTGCAAAACCTGATCAGGTGGAACCGAGAACTGAAATTA	2564
QY	2401	CAACTTTACAGGAGTGAATCAAGTGGCTTCAGAGGCACCAAGATTTTATCCCAAAATGG	2460
Db	2565	CAACTTTACAGGAGTGAATCAAGTGGCTTCAGAGGCACCAAGATTTTATCCCAAAATGG	2624
QY	2461	AGGGAATCCAAATTTGTTTATATCTGATGAAGAAGTGGTCCCGAAGAGACAGAGACAGAC	2520
Db	2625	AGGGAATCCAAATTTGTTTATATCTGATGAAGAAGTGGTCCCGAAGAGACAGAGACAGAC	2684
QY	2521	ACTTTTGATGCGCACCGGACGCTCGAGGGGAAGTGGCTTTGTCATCAGACTCTCTAAGG	2580

Db 2685 ACTTTGATGCGCGACGCGACCTGCGAGGGAAGCTGCTTTCATGACACTCTTAAGG 2744
Qy 2581 ACTGGAAGCTCAGCATATCTCAGACATTTGTAAGCAGAGAAATGACAGATGCCCTC 2640
Db 2745 ACTGGAAGCTCAGCATATCTCAGACATTTGTAAGCAGAGAAATGACAGATGCCCTC 2804
Qy 2641 AGCTTGCTCATGTCAAACTGAATAA 2667
Db 2805 AGCTTGCTCATGTCAAACTGAATAA 2831

RESULT 6
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROMNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOPF, VALENTIN K
; TITLE OF INVENTION: HUMAN KENOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 98.6%; Score 2630; DB 9; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

Qy 1 ATGAAGATGTGAGTGGGCGGGGAGAGGTGCTGTGAACCTGCGAGCGCGCCAGGGGC 60
Db 1 ATGAAGATGTGAGTGGGCGGGGAGAGGTGCTGTGAACCTGCGAGCGCGCCAGGGGC 60
Qy 61 GAGGCGCTGTACTGCTGTGGGCAACCGCGGCGGCGGCTTGTGGCGGCGGCGGCTG 120
Db 61 GAGGCGCTGTACTGCTGTGGGCAACCGCGGCGGCGGCTTGTGGCGGCGGCGGCTG 120
Qy 121 AGGGAAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 180
Db 121 AGGGAAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 180
Qy 181 TACACGAGTAGCAGACAGCTCCGCGGCAACGTCAAGTACCGGCGGCGGCGGCGGCT 240
Db 181 TACACGAGTAGCAGACAGCTCCGCGGCAACGTCAAGTACCGGCGGCGGCGGCGGCT 240
Qy 241 TACAACTGCTGAGAGAACCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 300
Db 241 TACAACTGCTGAGAGAACCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 300
Qy 301 CTGTGCTTGTGCTGCTGATTTTGTCAAGTCTTCAACATCCCTGAGCACAAATTTG 360
Db 301 CTGTGCTTGTGCTGCTGATTTTGTCAAGTCTTCAACATCCCTGAGCACAAATTTG 360
Qy 361 GCTCAAGTGTGCTTGTGATCTGAGATCTGATGATGATGATGATGATGATGATGAT 420
Db 361 GCTCAAGTGTGCTTGTGATCTGAGATCTGATGATGATGATGATGATGATGATGAT 420
Qy 421 ATCATTCGAAATCTGCTGCGGGGTGCTGTTCGATATAGAGGATGCGCAAGAAAGCTG 480
Db 421 ATCATTCGAAATCTGCTGCGGGGTGCTGTTCGATATAGAGGATGCGCAAGAAAGCTG 480

Qy 481 AGGTTTCTGGAAGCCCTTCTGTATATAGATACCATTTGCTTATACGCTTCAATAGCA 540
Db 481 AGGTTTCTGGAAGCCCTTCTGTATATAGATACCATTTGCTTATACGCTTCAATAGCA 540
Qy 541 GTTGTGTTCTGCAAAAACCTCAGGGTAATTTTGTGCAAGCTGCTCAGTCAAGCTTC 600
Db 541 GTTGTGTTCTGCAAAAACCTCAGGGTAATTTTGTGCAAGCTGCTCAGTCAAGCTTC 600
Qy 601 TTCTTCAGATCTCTCCGATGCGCATGAGACCGAAGGGGAGGCACTTGGAAATTAAT 660
Db 601 TTCTTCAGATCTCTCCGATGCGCATGAGACCGAAGGGGAGGCACTTGGAAATTAAT 660
Qy 661 GATTCAAGTGTATGCTCAGACAGAAATTAATCAAGCTTGTATAGATAGATTTTGG 720
Db 661 GATTCAAGTGTATGCTCAGACAGAAATTAATCAAGCTTGTATAGATAGATTTTGG 720
Qy 721 GTTCTTATTTTGTGCTTCTTCTGCTATCTGTGTAAGAAAGATGCCAATTAAGATT 780
Db 721 GTTCTTATTTTGTGCTTCTTCTGCTATCTGTGTAAGAAAGATGCCAATTAAGATT 780
Qy 781 TCTACATATGACAGATCTCTGTGTGGGCAATTAATGCAATTAATGCTATGGA 840
Db 781 TCTACATATGACAGATCTCTGTGTGGGCAATTAATGCAATTAATGCTATGGA 840
Qy 841 GACAAAACCTCCCTAATGCTGCTGGAAGATTTCTTGTGCAAGCTTGTGCACTTGGC 900
Db 841 GACAAAACCTCCCTAATGCTGCTGGAAGATTTCTTGTGCAAGCTTGTGCACTTGGC 900
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Db 901 ATTTCTTTCTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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Db 961 GAACAACACCGCGAGAAACATTTGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
Qy 1021 TGTGTTTGGCGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Db 1021 TGTGTTTGGCGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Qy 1081 CACTTGAAGGCTTGTGCAACCTGACGCTTACCA----- 1115
Db 1081 CACTTGAAGGCTTGTGCAACCTGACGCTTACCA----- 1115
Qy 1116 --TCAGAGCTAAGTTTAAGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1173
Db 1116 --TCAGAGCTAAGTTTAAGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1173
Qy 1141 AGTCAGAGCTAAGTTTAAGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1141 AGTCAGAGCTAAGTTTAAGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Qy 1174 AAGAGCCGACAGGCTCAGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1233
Db 1201 AAGAGCCGACAGGCTCAGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Qy 1234 GGCAGTCCACCAAGAGTGCAGAAAGCTGAGCTTCAACGACGAAACCGCTTCCGCGCC 1293
Db 1261 GGCAGTCCACCAAGAGTGCAGAAAGCTGAGCTTCAACGACGAAACCGCTTCCGCGCC 1320
Qy 1294 TCGCTGCGGCTCAAAAGTTCTCAGCCCAAAACAGTATGATGATGATGATGATGAT 1353
Db 1321 TCGCTGCGGCTCAAAAGTTCTCAGCCCAAAACAGTATGATGATGATGATGATGAT 1380
Qy 1354 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
Db 1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
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Db 1501 AAGTTTAAGAAACGTTAGCTCATATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 1534 GGTCACTGGAATGTTGTGAGAAATTAAGACCTTCAAAACAGTGTGATCAAAATTTCT 1593

DB 1561 GGTCATCTGGACATGTTGTGTAGAAATTAAGCCCTCAAAACAGTGTGATCAAAATTCCT 1620
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DB 1621 GGAAGAGGGGAATTCATCAGATTAAGAGAGCCGAGAGAAATTAACAGAGAACATGAG 1680
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DB 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAAGAGTACAGTCC 1740
QY 1714 ATAGAGTCCAGGTGAGTGGCTCTACTAGACATCTATCAACAGGTCTCTTGGAAGGCTCT 1773
DB 1741 ATAGAGTCCAGGTGAGTGGCTCTACTAGACATCTATCAACAGGTCTCTTGGAAGGCTCT 1800
QY 1774 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTGAATGTAAGAGACATCT 1833
DB 1801 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTGAATGTAAGAGACATCT 1860
QY 1834 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGC 1893
DB 1861 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGC 1920
QY 1894 TTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTTGAGTTCACTTGACGCCAAT 1953
DB 1921 TTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTTGAGTTCACTTGACGCCAAT 1980
QY 1954 GAGTTGAGTGGCCAGACTTCTCAAGGCTTGAAGCCCTACTATGACAGTCAAGCAACAG 2013
DB 1981 GAGTTGAGTGGCCAGACTTCTCAAGGCTTGAAGCCCTACTATGACAGTCAAGCAACAG 2040
QY 2014 GTGCCAATTAGTCAAAAGCATGGCTCAGACAGTGGCAACCAACCACTTGCAACCA 2073
DB 2041 GTGCCAATTAGTCAAAAGCATGGCTCAGACAGTGGCAACCAACCACTTGCAACCA 2100
QY 2074 ATAAATACGGCAACCCAGGCAAGCCCAACCACTTTACAGATGCCACCTCCTCCCA 2133
DB 2101 ATAAATACGGCAACCCAGGCAAGCCCAACCACTTTACAGATGCCACCTCCTCCCA 2160
QY 2134 GCCATCAAGCATCTGCCAGGCAAGAACTCTGCAACCTTACAGGCTTACAGAA 2193
DB 2161 GCCATCAAGCATCTGCCAGGCAAGAACTCTGCAACCTTACAGGCTTACAGAA 2220
QY 2194 AGCATTTCTGAGCTCAACACTGCTCTTGTTCCTCAAGAGAAATGTTGAGTGCAG 2253
DB 2221 AGCATTTCTGAGCTCAACACTGCTCTTGTTCCTCAAGAGAAATGTTGAGTGCAG 2280
QY 2254 TCAAACTCTACCAAGGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAGAACTG 2313
DB 2281 TCAAACTCTACCAAGGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAGAACTG 2340
QY 2314 TTGTCTGTCTGCTCCATGCTGCGAAGAGACTTGGGCAAACTTTGTCTGTGCAAACTG 2373
DB 2341 TTGTCTGTCTGCTCCATGCTGCGAAGAGACTTGGGCAAACTTTGTCTGTGCAAACTG 2400
QY 2374 ATCAGGTCGACCGAGAACTGAATATACAACTTTGAGGAGTGAAGTCAAGTGGCTCCA 2433
DB 2401 ATCAGGTCGACCGAGAACTGAATATACAACTTTGAGGAGTGAAGTCAAGTGGCTCCA 2460
QY 2434 GGCAGCCAGATTTTAAACCCAAATGAGAGGAAATCCAAATGTTTAACTGATGAAG 2493
DB 2461 GGCAGCCAGATTTTAAACCCAAATGAGAGGAAATCCAAATGTTTAACTGATGAAG 2520
QY 2494 GTGGGTCGCCAAGAGACAGAGACAGACTTTTGTATGCGCACCCGAGGCTGCGAGGAA 2553
DB 2521 GTGGGTCGCCAAGAGACAGAGACAGACTTTTGTATGCGCACCCGAGGCTGCGAGGAA 2580
QY 2554 GCTGCTTTGATCAGACTCTCTTAAGAGCTGGAAGTCAAGATCATCTCAGAGCAATTTGT 2613
DB 2581 GCTGCTTTGATCAGACTCTCTTAAGAGCTGGAAGTCAAGATCATCTCAGAGCAATTTGT 2640
QY 2614 AAGGCAAGAAAGTACAGATGCCCTCAGTTGCTCATGTCAAACTGAATTA 2667

DB 2641 AAGCAGAGAGAAATGACAGATGCCCCCTCAGCTTGCCCTCATGTCAAACTGAATTA 2694
RESULT 7
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCON5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCON5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCON5-1
US-09-810-796-2
Query Match 98.6%; Score 2630; DB 9; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
QY 1 ATGAAGATGTGAGTGTGCGGCGCGGCGAGGGGCTGTAACCTGCGGCGCGGCGAGGCG 60
DB 1 ATGAAGATGTGAGTGTGCGGCGCGGCGAGGGGCTGTAACCTGCGGCGCGGCGAGGCG 60
QY 61 GACGCGCTGTACTACTGCTGGGACACCGCGCGGCAAGCTTGTGTGGCGCGGCGGCTG 120
DB 61 GACGCGCTGTACTACTGCTGGGACACCGCGCGGCAAGCTTGTGTGGCGCGGCGGCTG 120
QY 121 AGGAGAGCCCGCGGCGCAAGCGGGGCGCGGATGAGCTGTGGGGAAGCCGCTCT 180
DB 121 AGGAGAGCCCGCGGCGCAAGCGGGGCGCGGATGAGCTGTGGGGAAGCCGCTCT 180
QY 121 AGGAGAGCCCGCGGCGCAAGCGGGGCGCGGATGAGCTGTGGGGAAGCCGCTCT 180
DB 121 AGGAGAGCCCGCGGCGCAAGCGGGGCGCGGATGAGCTGTGGGGAAGCCGCTCT 180
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DB 181 TACAGAGTACGACGAGCTGCGCGGCAAGCTCAAGTACCGGCGGCGTCAAGACTACCTG 240
QY 241 TACACGTGCTGAGAGACCCCGCGGCTGGGCGTTGATCTACACAGCTTGTGTTTCTC 300
DB 241 TACACGTGCTGAGAGACCCCGCGGCTGGGCGTTGATCTACACAGCTTGTGTTTCTC 300
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DB 301 CTGTGCTTTGGTGTGTTATTTTGTCAAGTGTCTTACATCCCTGAGACACAAATTTG 360
QY 361 GCCTCAAGTGGCTCTTGAATCTGAGTTCGTAATGTTGTGCTTGTGTTGAGTTTC 420
DB 361 GCCTCAAGTGGCTCTTGAATCTGAGTTCGTAATGTTGTGCTTGTGTTGAGTTTC 420
QY 421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGCTGATATAGAGATGCGAAGAACTG 480
DB 421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGCTGATATAGAGATGCGAAGAACTG 480
QY 481 AGGTTGCTCGAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 540
DB 481 AGGTTGCTCGAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 540
QY 541 GTTGTTCGCAAAAACCTCAGGCTTAATTTTGTGCAAGTCTGCAAGTCTCCGT 600
DB 541 GTTGTTCGCAAAAACCTCAGGCTTAATTTTGTGCAAGTCTGCAAGTCTCCGT 600

QY	601	TTCCATCAGATCTCCCGATGGTGGCATATGCA	CCGAAGGGAGGCATTTGAAATTACTG	660
Db	601	TTCCATCAGATCTCCCGATGGTGGCATATGCA	CCGAAGGGAGGCATTTGAAATTACTG	660
QY	661	GGTTCAGTGGTTATGCTCACAGCAAGGAATTAA	TACAGAGCTTGGTACATAGATTTTGTG	720
Db	661	GGTTCAGTGGTTATGCTCACAGCAAGGAATTAA	TACAGAGCTTGGTACATAGATTTTGTG	720
QY	721	GTTCTTATTTTTTGGCTTTCTTGTCTATCTG	TGTGGAAAGATGCGAATPAAGATTT	780
Db	721	GTTCTTATTTTTTGGCTTTCTTGTCTATCTG	TGTGGAAAGATGCGAATPAAGATTT	780
QY	781	TCTACATATGCAATGCTCTGTGGGGGCAAA	TTAATCATTTGACAACTATTGGCTATGGA	840
Db	781	TCTACATATGCAATGCTCTGTGGGGGCAAA	TTAATCATTTGACAACTATTGGCTATGGA	840
QY	841	GACAAATCTCCCTTACTTGGCTGGAAAGATT	CTTTGTGACAGCTTTGCACTCCCTTGGC	900
Db	841	GACAAATCTCCCTTACTTGGCTGGAAAGATT	CTTTGTGACAGCTTTGCACTCCCTTGGC	900
QY	901	ATTTCCTTCTTGGCACTTCCTGGCCGGCA	TTCTTGGCTCAAGTTTGGCATTTAAAGTACA	960
Db	901	ATTTCCTTCTTGGCACTTCCTGGCCGGCA	TTCTTGGCTCAAGTTTGGCATTTAAAGTACA	960
QY	961	GAACAACAACCGCCACAGAAA	CACTTTGAGAAAAGAAAGAACCCAGCTGCCAA	1020
Db	961	GAACAACAACCGCCACAGAAA	CACTTTGAGAAAAGAAAGAACCCAGCTGCCAA	1020
QY	1021	TGTGTTTGGCTGATTAACGACAGCTGATAGA	AAATCTGTTTCCATTGCAACCTGGAAGCA	1080
Db	1021	TGTGTTTGGCTGATTAACGACAGCTGATAGA	AAATCTGTTTCCATTGCAACCTGGAAGCA	1080
QY	1081	CACTTGAAAGGCGCTTGCA	CACTGCGACGCTTGCA-----	1145
Db	1081	CACTTGAAAGGCGCTTGCA	CACTGCGACGCTTGCA-----	1145
QY	1145	--TCAGAAAGCTTAAGTTTAAAGAGCGAG	TGCGCATGAGCTTACCCGAGGGCCAGATATT	1200
Db	1145	--TCAGAAAGCTTAAGTTTAAAGAGCGAG	TGCGCATGAGCTTACCCGAGGGCCAGATATT	1200
QY	1174	AAGAGCCGACAAAGCTCAGTAGTAGTCA	AGAGAGTCCCAACGACATCAACGCCGAG	1233
Db	1201	AAGAGCCGACAAAGCTCAGTAGTAGTCA	AGAGAGTCCCAACGACATCAACGCCGAG	1260
QY	1234	GGCAGTCCCAACAAAGTGCAGAAAGAGCTT	CAACGACCGAACCCGCTTCCGGGCC	1293
Db	1261	GGCAGTCCCAACAAAGTGCAGAAAGAGCTT	CAACGACCGAACCCGCTTCCGGGCC	1320
QY	1294	TGCGTGGCGCTCAAAAGTTCTCAGCCAAA	CCAGATAGATGCTGCACAGCCCTTGGC	1353
Db	1321	TGCGTGGCGCTCAAAAGTTCTCAGCCAAA	CCAGATAGATGCTGCACAGCCCTTGGC	1380
QY	1354	ACTGATGATGTATATGATGAAAAAGAA	AGCAAGTGTATGTATCAGTGGAAAGACTCAC	1413
Db	1381	ACTGATGATGTATATGATGAAAAAGAA	AGCAAGTGTATGTATCAGTGGAAAGACTCAC	1440
QY	1414	CCACCACTTAAACGTCTCATTCGAGCTAT	CGAAATTATGAATTTCAATGTTGCAAAACGG	1473
Db	1441	CCACCACTTAAACGTCTCATTCGAGCTAT	CGAAATTATGAATTTCAATGTTGCAAAACGG	1500
QY	1474	AAGTTTAAAGGAACGTTTACGTTCCATAT	GTATATGTTGAACAATATTCTGCT	1533
Db	1501	AAGTTTAAAGGAACGTTTACGTTCCATAT	GTATATGTTGAACAATATTCTGCT	1560
QY	1534	GGTCATCTGACATGTTGTGTAGATTAAAG	CCCTTCAACACGCTGTGATCAATATTCTT	1593
Db	1561	GGTCATCTGACATGTTGTGTAGATTAAAG	CCCTTCAACACGCTGTGATCAATATTCTT	1620
QY	1594	GGAAAAAGGCAATCATCATGATPAGAGAG	CCGAGAGAAATPACAGCAGAAATCATGAG	1653
Db	1621	GGAAAAAGGCAATCATCATGATPAGAGAG	CCGAGAGAAATPACAGCAGAAATCATGAG	1680

OY	1654	ACCAACAGACATCTCAGTATGCTCGGTCCGGTGTCAAAGTTGAAAACAGGTACAGTCC	1713
Db	1661	ACCAACAGACATCTCAGTATGCTCGGTCCGGTGTCAAAGTTGAAAACAGGTACAGTCC	1740
OY	1714	ATTAAGTCCAAAGCTGCACTGCTACTAAGACATATATCAACAGATCCTTCGAAAAGGCTCT	1773
Db	1741	ATTAGATCCAAAGCTGCACTGCTACTAAGACATATATCAACAGATCCTTCGAAAAGGCTCT	1800
OY	1774	GCCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCACCTTTTGAATGTGAACAGACATCT	1833
Db	1801	GCCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCACCTTTTGAATGTGAACAGACATCT	1860
OY	1834	GACATATCAAAGCCCTGTGGATACCAAAAGATCTTTGGGTTCCGCACAAAACAGTGGCTGC	1893
Db	1861	GACATATCAAAGCCCTGTGGATACCAAAAGATCTTTGGGTTCCGCACAAAACAGTGGCTGC	1920
OY	1894	TTATCCAGATCAACTAGTGGCAACATCTGGAAGGGCTGACGTTCAATCTGACGCCAAT	1953
Db	1921	TTATCCAGATCAACTAGTGGCAACATCTGGAAGGGCTGACGTTCAATCTGACGCCAAT	1980
OY	1954	GAGTTCAGTGSCCAAGACTTTCTACGGCGCTTAAGCCCTACTATCAACAGTCMAAGCACAG	2013
Db	1981	GAGTTCAGTGSCCAAGACTTTCTACGGCGCTTAAGCCCTACTATCAACAGTCMAAGCACAG	2040
OY	2014	GTCGCCAATTGTGTCMAAGCCGATGGCTCAGACGTGGCAGCCACCAACCATTTGCCAACCA	2073
Db	2041	GTCGCCAATTGTGTCMAAGCCGATGGCTCAGACGTGGCAGCCACCAACCATTTGCCAACCA	2100
OY	2074	ATTAATAGGCGACCCCAAGCAGAGGCCCAACCAACTTACATATCCACTCCCTCCCA	2133
Db	2101	ATTAATAGGCGACCCCAAGCAGAGGCCCAACCAACTTACATATCCACTCCCTCCCA	2160
OY	2134	GCCATCAAGACATCTGCCACAGGCCAGAACTCTGCACCTTAACCCCTGCAGGCTTACAGAA	2193
Db	2161	GCCATCAAGACATCTGCCACAGGCCAGAACTCTGCACCTTAACCCCTGCAGGCTTACAGAA	2220
OY	2194	AGCATTTCTGACGTCAACCACTGCTGTGGCTTCCAGAGAAATGTTCAGTTGCACAG	2253
Db	2221	AGCATTTCTGACGTCAACCACTGCTGTGGCTTCCAGAGAAATGTTCAGTTGCACAG	2280
OY	2254	TCAAATCTCAACCAAGACCGTTCTATAGAGAAAAGCTTTGAATGGAGAGAAACTCTG	2313
Db	2281	TCAAATCTCAACCAAGACCGTTCTATAGAGAAAAGCTTTGAATGGAGAGAAACTCTG	2340
OY	2314	TTGTCCTGTCTGTCCCAATGGTCCGAAGACTTGGGCAAACTTTGTCTGTGCAAAACTG	2373
Db	2341	TTGTCCTGTCTGTCCCAATGGTCCGAAGACTTGGGCAAACTTTGTCTGTGCAAAACTG	2400
OY	2374	ATCAGGTGACCCGAGAACTGAATATACAACTTTCAGGAGTGAAGTCAAGTGCCTCAGA	2433
Db	2401	ATCAGGTGACCCGAGAACTGAATATACAACTTTCAGGAGTGAAGTCAAGTGCCTCAGA	2460
OY	2434	GGCAGCCCAAAATTTTATACCCCAAAATGGAGGAAATCCAATTTGTTATATCTGATGAAG	2493
Db	2461	GGCAGCCCAAAATTTTATACCCCAAAATGGAGGAAATCCAATTTGTTATATCTGATGAAG	2520
OY	2494	GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGAATGCCGACCGCAGCCTGGCCAGGGAA	2553
Db	2521	GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGAATGCCGACCGCAGCCTGGCCAGGGAA	2580
OY	2554	GCTGCTTTGTCATCAGACTCTCTAAAGACTGGAAAGTCAAGATCATCTTCAGAGCATTTGT	2613
Db	2581	GCTGCTTTGTCATCAGACTCTCTAAAGACTGGAAAGTCAAGATCATCTTCAGAGCATTTGT	2640
OY	2614	AAAGCAGAGAAAGTACAGATGCTCTCAGCTTGCCTCATGTCAAACTGAATTA	2667
Db	2641	AAAGCAGAGAAAGTACAGATGCTCTCAGCTTGCCTCATGTCAAACTGAATTA	2694

Db	1801	GCCTAGCCCTTGGCTTTCATTCAGATCCACCTTTGAAATGAAACAGACATCT	1860
Qy	1834	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGCGGTTCCGACAAAGAGTGGCTGC	1893
Db	1861	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGCGGTTCCGACAAAGAGTGGCTGC	1920
Qy	1894	TTATTCAGATCAATAGTGCACATCTTCGAGAGGCTTCGAGTTCAATCTGACGCCAAT	1953
Db	1921	TTATTCAGATCAATAGTGCACATCTTCGAGAGGCTTCGAGTTCAATCTGACGCCAAT	1980
Qy	1954	GAGTTCAATGCGCCACATTTCTGAGCGCTTGAAGCCCTACTATGACAGTCAAGCAACAG	2013
Db	1961	GAGTTCAATGCGCCACATTTCTGAGCGCTTGAAGCCCTACTATGACAGTCAAGCAACAG	2040
Qy	2014	GTGCAATTAAGTCAAAAGCATGCTCAGCAGTGCAGGACACCAACCATTTGCAACCA	2073
Db	2041	GTGCAATTAAGTCAAAAGCATGCTCAGCAGTGCAGGACACCAACCATTTGCAACCA	2100
Qy	2074	ATTAATACGGCAGCCCAAGCCAGAGCCCAACCACTTTACAGATCCACTCTCTCCA	2133
Db	2101	ATTAATACGGCAGCCCAAGCCAGAGCCCAACCACTTTACAGATCCACTCTCTCCA	2160
Qy	2134	GCCATTCAGCATCTGCGCCAGGCGCAAACTCTGCACCTTAACCTTCGAGGCTTACAGAA	2193
Db	2161	GCCATTCAGCATCTGCGCCAGGCGCAAACTCTGCACCTTAACCTTCGAGGCTTACAGAA	2220
Qy	2194	AGCATTTCTGACGTACACCACTGCTTGTGGCTTCAAGAAATGTTCAGTTGTCACAG	2253
Db	2221	AGCATTTCTGACGTACACCACTGCTTGTGGCTTCAAGAAATGTTCAGTTGTCACAG	2280
Qy	2254	TCAATCTCACCAAGAGCCGTTCTATGAGAAAGCTTTGA CATGGAAGAGAACTGTG	2313
Db	2281	TCAATCTCACCAAGAGCCGTTCTATGAGAAAGCTTTGA CATGGAAGAGAACTGTG	2340
Qy	2314	TTGTCTGTCTGTCCATAGTGTGCGCAAGCATTTGGCAATCTTTGTCTGTGCCAAACCTG	2373
Db	2341	TTGTCTGTCTGTCCATAGTGTGCGCAAGCATTTGGCAATCTTTGTCTGTGCCAAACCTG	2400
Qy	2374	ATCAGGTGACCGAGAGAACTGAATTATACATTTTCAGGAGTGAAGTCAAGTGGCTCCAGA	2433
Db	2401	ATCAGGTGACCGAGAGAACTGAATTATACATTTTCAGGAGTGAAGTCAAGTGGCTCCAGA	2460
Qy	2434	GCGAGCCAGATTTTATCCCAATGAGGGAAATCCAAATTTGTTATTAATCTGATGAAG	2493
Db	2461	GCGAGCCAGATTTTATCCCAATGAGGGAAATCCAAATTTGTTATTAATCTGATGAAG	2520
Qy	2494	GTGGGTCCCGAAGACAGACAGACACTTTTGAATGCCGACCGCAGCTTCGACGGGAA	2553
Db	2521	GTGGGTCCCGAAGACAGACAGACACTTTTGAATGCCGACCGCAGCTTCGACGGGAA	2580
Qy	2554	GCTGCTTTGATCAGACTCTCTAAGAGCTGGAAGTCAAGATCATCTCAGAGCATTTGT	2613
Db	2581	GCTGCTTTGATCAGACTCTCTAAGAGCTGGAAGTCAAGATCATCTCAGAGCATTTGT	2640
Qy	2614	AAGCAGAGAGAAATGACAGATGCTCCTCAGCTTGCTCATGTCAACTGAATTA 2667	
Db	2641	AAGCAGAGAGAAATGACAGATGCTCCTCAGCTTGCTCATGTCAACTGAATTA 2694	
RESULT 9			
US-09-810-796-1			
: Sequence 1, Application US/09810796			
: Patent No. US20020102677A1			
: GENERAL INFORMATION:			
: APPLICANT: Jegle, Timothy James			
: APPLICANT: ICAGEN, Inc.			
: TITLE OF INVENTION: KCU05, a No. US20020102677A1 Polaeasium Channel			
: FILE REFERENCE: 018512-005010US			
: CURRENT APPLICATION NUMBER: US/09/810,796			
: CURRENT FILING DATE: 2001-10-12			
: PRIOR APPLICATION NUMBER: US 60/190,954			
: PRIOR FILING DATE: 2000-03-21			

[illegible]

QY 841 GACAAAATCTCCCTAACTTGGCTGGGAGATTGCTTTCTGACAGCTTTGCACTCTTGGC 900
Db 850 GACAAAATCTCCCTAACTTGGCTGGGAGATTGCTTTCTGACAGCTTTGCACTCTTGGC 909
QY 901 ATTTCTTTCTTTGCACTTCTGCGGGCATTTCTGGCTCAGTTTTCATTTAAAGTACA 960
Db 910 ATTTCTTTCTTTGCACTTCTGCGGGCATTTCTGGCTCAGTTTTCATTTAAAGTACA 969
QY 961 GAACAACCGCGAGAAACATTTGAGAAAGAGAACCCAGCTCCAACTCATTTAG 1020
Db 970 GAACAACCGCGAGAAACATTTGAGAAAGAGAACCCAGCTCCAACTCATTTAG 1029
QY 1021 TGTGTTGGCGTAACTGACAGCTGATGAGAAATCTGTTTCATTGCAACTTGAAGCA 1080
Db 1030 TGTGTTGGCGTAACTGACAGCTGATGAGAAATCTGTTTCATTGCAACTTGAAGCA 1089
QY 1081 CACTTGAAGGCTTTGACACCTGACAGCTCCACCA----- 1115
Db 1090 CACTTGAAGGCTTTGACACCTGACAGCTCCACCA----- 1149
QY 1116 --TCAGAACTAAGTTTAAAGACGAGTGCATGCTAGCCCAAGGGCCAGATATT 1173
Db 1150 AGTCABAAGTAAAGTTTAAAGACGAGTGCATGCTAGCCCAAGGGCCAGATATT 1209
QY 1174 AAGAGCCGACAAAGCTCAGTAGGTGA CAGAGGTTCCCAAGCA CCGACATCAAGCCGAG 1233
Db 1210 AAGAGCCGACAAAGCTCAGTAGGTGA CAGAGGTTCCCAAGCA CCGACATCAAGCCGAG 1269
QY 1234 GGCAGTCCCAACCAAGTGAAGAGTGGAGTTCAGACGACCGGCTTCGCGCC 1293
Db 1270 GGCAGTCCCAACCAAGTGAAGAGTGGAGTTCAGACGACCGGCTTCGCGCC 1329
QY 1294 TCGCTCGGCTCAAAAGTTCTCAGCCAAACAGTATAGTGTGACACAGCCCTTGGC 1353
Db 1330 TCGCTCGGCTCAAAAGTTCTCAGCCAAACAGTATAGTGTGACACAGCCCTTGGC 1389
QY 1354 ACTGATGATGATATGATGAAAAAGATGCGCAGTGTGATGATCAGTGAAGACTCTAC 1413
Db 1390 ACTGATGATGATATGATGAAAAAGATGCGCAGTGTGATGATCAGTGAAGACTCTAC 1449
QY 1414 CCACCACTTAAACCTGCAATGAGCTATCAGAAATTATGAAATTTCAATGTCMAAAGG 1473
Db 1450 CCACCACTTAAACCTGCAATGAGCTATCAGAAATTATGAAATTTCAATGTCMAAAGG 1509
QY 1474 AAGTTTAAAGAAAGTTTACGTCCATATGATGTAAGAAAGATGTCATTGAAACATATTCGT 1533
Db 1510 AAGTTTAAAGAAAGTTTACGTCCATATGATGTAAGAAAGATGTCATTGAAACATATTCGT 1569
QY 1534 GGTCACTGTGACATGTTGTGTAGATTAAAGCCTTCAACACGTGTGATCAAAATTTCT 1593
Db 1570 GGTCACTGTGACATGTTGTGTAGATTAAAGCCTTCAACACGTGTGTATCAAAATTTCT 1629
QY 1594 GGAAGAGGCAATCATCAGATTAAGAAAGCCGAGAGAAATTAACACAGACATGAG 1653
Db 1630 GGAAGAGGCAATCATCAGATTAAGAAAGCCGAGAGAAATTAACACAGACATGAG 1689
QY 1654 ACCACAGACATCTCAGTAGTCTCGGTGCGGTGTCAGAGTTGAAAAA CAGGTACAGTCC 1713
Db 1690 ACCACAGACATCTCAGTAGTCTCGGTGCGGTGTCAGAGTTGAAAAA CAGGTACAGTCC 1749
QY 1714 ATAGAGTCCAGGTGAGCTGCTACTAGACATCTATCAACAGGTCTTTGGAAAGGCTCT 1773
Db 1750 ATAGAGTCCAGGTGAGCTGCTACTAGACATCTATCAACAGGTCTTTGGAAAGGCTCT 1809
QY 1774 GCTCAGCCCTGCTTTGGCTTCAATCCAGATCCGCTTTGAAATGTAACAGACATCT 1833
Db 1810 GCTCAGCCCTGCTTTGGCTTCAATCCAGATCCGCTTTGAAATGTAACAGACATCT 1869
QY 1834 GACTATCAAGCCCTGTGATGACAAAGATCTTTGCGGTTCCGACAAACAGTGGCTGC 1893
Db 1870 GACTATCAAGCCCTGTGATGACAAAGATCTTTGCGGTTCCGACAAACAGTGGCTGC 1929

QY 1894 TTATCCAGATCACTAGTCCCAACATCTTCGAGAGGCTTCAGATTCTGACGCCAAAT 1953
Db 1930 TTATCCAGATCACTAGTCCCAACATCTTCGAGAGGCTTCAGATTCTGACGCCAAAT 1989
QY 1954 GAGTTCAGTCCCAACATTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2013
Db 1990 GAGTTCAGTCCCAACATTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2049
QY 2014 GTGCCAATTTAGTCAAGGAGATGCTCAGACAGTGCAGGCCACCAACCAATTGCAACCA 2073
Db 2050 GTGCCAATTTAGTCAAGGAGATGCTCAGACAGTGCAGGCCACCAACCAATTGCAACCA 2109
QY 2074 ATAAATACGGACCCCAAGCCAGACGCCCAACCACTTTACAGATCCACTCTCTCCA 2133
Db 2110 ATAAATACGGACCCCAAGCCAGACGCCCAACCACTTTACAGATCCACTCTCTCCA 2169
QY 2134 GCCATCAAGACATTCGCCAGGCGAGAAACCTGCAACCCCTTAACCCCTGAGGCTTACAGGA 2193
Db 2170 GCCATCAAGACATTCGCCAGGCGAGAAACCTGCAACCCCTTAACCCCTGAGGCTTACAGGA 2229
QY 2194 AGCATTTCTGACGTACCAACCTGCTGTTGCTTCAGAGAAATGTTCAAGTTGACAG 2253
Db 2230 AGCATTTCTGACGTACCAACCTGCTGTTGCTTCAGAGAAATGTTCAAGTTGACAG 2289
QY 2254 TCAAAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGAGAGAACTCTG 2313
Db 2290 TCAAAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGAGAGAACTCTG 2349
QY 2314 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2373
Db 2350 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2409
QY 2374 ATCAGGTGACCGAGAACTGAATATCACTTTTCAAGGAGTGAATCAAGTGCCTCAGA 2433
Db 2410 ATCAGGTGACCGAGAACTGAATATCACTTTTCAAGGAGTGAATCAAGTGCCTCAGA 2469
QY 2434 GGCAGCCAAAGTTTACCACCAATGAGGAAATGCAAAATGTTTATTAATCATGATAAG 2493
Db 2470 GGCAGCCAAAGTTTACCACCAATGAGGAAATGCAAAATGTTTATTAATCATGATAAG 2529
QY 2494 GTGGGTCCGAGAGACAGACAGACACTTTTGAATGCGGACCGGACCTGCGAGGAA 2553
Db 2530 GTGGGTCCGAGAGACAGACAGACACTTTTGAATGCGGACCGGACCTGCGAGGAA 2589
QY 2554 GCTGCTTTGATCAGACTCTCTAAGACCTGAAAGTCAAGATCTCAGAGCAATTGT 2613
Db 2590 GCTGCTTTGATCAGACTCTCTAAGACCTGAAAGTCAAGATCTCAGAGCAATTGT 2649
QY 2614 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCMAACTGAATTA 2667
Db 2650 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCMAACTGAATTA 2703

RESULT 10
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2615-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Query Match 98.4%; Score 2625.2; DB 19; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAGAGATGTGAGTGGGCGGGGAGGGTGTCTGTGAACCTCGGACCGCGAGGGGC 60
DB 1 ATGAGAGATGTGAGTGGGCGGGGAGGGTGTCTGTGAACCTCGGACCGCGAGGGGC 60
QY 61 GAGGCGCTGTAAGTCTGGGCAACCGGCGGCAAGCTTGTGGCGGCGGCGGTGGCCTG 120
DB 61 GAGGCGCTGTAAGTCTGGGCAACCGGCGGCAAGCTTGTGGCGGCGGCGGTGGCCTG 120
QY 121 AGGAGAGCGCGCGGGGCAAGAGGGGGCCCGATGAGCTGTGGGGAAGCCGCTCT 180
DB 121 AGGAGAGCGCGCGGGGCAAGAGGGGGCCCGATGAGCTGTGGGGAAGCCGCTCTCT 180
QY 181 TACACGAGTACGCAAGCTCCGCGCAAGTCAAGTCCGCGGAGTGCAGAACTACCTG 240
DB 181 TACACGAGTACGCAAGCTCCGCGCAAGTCAAGTCCGCGGAGTGCAGAACTACCTG 240
QY 241 TACAGCGTGTGAGAGACCCCGCGGTGGCGCTTCACTACAGCTTTCGTTTTCTC 300
DB 241 TACAGCGTGTGAGAGACCCCGCGGTGGCGCTTCACTACAGCTTTCGTTTTCTC 300
QY 301 CTGTCTTTGGTGTGATTTTGTCAAGTCTTCTACATCCCTGAGCACAAGAAATG 360
DB 301 CTGTCTTTGGTGTGATTTTGTCAAGTCTTCTACATCCCTGAGCACAAGAAATG 360
QY 361 GCCTCAAGTTCCTTTGATCTGAGATTCGTGATGTTGCTTTGGTTTGAAGTTC 420
DB 361 GCCTCAAGTTCCTTTGATCTGAGATTCGTGATGTTGCTTTGGTTTGAAGTTC 420
QY 421 ATCATTCGATCTGTGTGGGGGTGTCTTTCGATATGAGATGCGCAAGAAAGCTG 480
DB 421 ATCATTCGATCTGTGTGGGGGTGTCTTTCGATATGAGATGCGCAAGAAAGCTG 480
QY 481 AGGTTTGTCTGAAAGCCCTCTGTGATATGATACCATTTGCTTATCGCTTCAATAGCA 540
DB 481 AGGTTTGTCTGAAAGCCCTCTGTGATATGATACCATTTGCTTATCGCTTCAATAGCA 540
QY 541 GTTGTCTTCTGCAAAATCTCAGGGTAATATTTTTCAGCGTCTGCACTCAGAACTTCCTG 600
DB 541 GTTGTCTTCTGCAAAATCTCAGGGTAATATTTTTCAGCGTCTGCACTCAGAACTTCCTG 600
QY 601 TTCTTACAGATCTCTCCGATGTGTGCGCATGGAACGAAAGGAGCACTTGAATTAATCTG 660
DB 601 TTCTTACAGATCTCTCCGATGTGTGCGCATGGAACGAAAGGAGCACTTGAATTAATCTG 660
QY 661 GGTTCAGTGTATATGCTCAGCAAGAAATTAATCAGCTTGTGATAGGATTTTGG 720
DB 661 GGTTCAGTGTATATGCTCAGCAAGAAATTAATCAGCTTGTGATAGGATTTTGG 720
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DB 721 GTTCTTATTTTTCGTCTTCTTCTGTCTATCTGTGTGAAAAAGATGCAATTAAGAGTTT 780
QY 781 TCTACATATGCAAGTCTCTGTGTGGGCAATTAATTAATTAATTAATTAATTAATTAATTA 840
DB 781 TCTACATATGCAAGTCTCTGTGTGGGCAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 841 GACAAAATCTCCCTTAACTTGGCTGGAAGATGCTTCTGAGGCTTTTGAATCTCTTGGC 900
DB 841 GACAAAATCTCCCTTAACTTGGCTGGAAGATGCTTCTGAGGCTTTTGAATCTCTTGGC 900
QY 901 ATTTCTTTCTTTGCACTTCTGCGGCAATTTTGGCTCAAGTTTGAATTAAGTACAA 960
DB 901 ATTTCTTTCTTTGCACTTCTGCGGCAATTTTGGCTCAAGTTTGAATTAAGTACAA 960
QY 961 GAACAAACCGGCGGAAACCTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
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QY 1021 TGTGTTTGGCGATGATACGACGCTGATGAGAAATCTGTTTCAATTCGAACTTGAAGCCA 1080
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QY 1081 CACTTGAAGGCTTGGACACTTGCAGCCCTTACCA----- 1115
DB 1081 CACTTGAAGGCTTGGACACTTGCAGCCCTTACCA----- 1115
QY 1116 --TCAGAGCTAAGTTTAAAGAGCGATGCGCATGCTAGCCCGAGGGGCGCAAGATATT 1173
DB 1116 --TCAGAGCTAAGTTTAAAGAGCGATGCGCATGCTAGCCCGAGGGGCGCAAGATATT 1173
QY 1174 AAGAGCGCAAGAGCTCAGTAGGTGAACAGAGGTCCCAAGACCGACATCAAGCCGAG 1233
DB 1174 AAGAGCGCAAGAGCTCAGTAGGTGAACAGAGGTCCCAAGACCGACATCAAGCCGAG 1233
QY 1201 AAGAGCGCAAGAGCTCAGTAGGTGAACAGAGGTCCCAAGACCGACATCAAGCCGAG 1260
DB 1201 AAGAGCGCAAGAGCTCAGTAGGTGAACAGAGGTCCCAAGACCGACATCAAGCCGAG 1260
QY 1234 GGCAGTCCCAACCAAGTGCAGAAAGAGCTGAGCTTCAACGACCGAAACCCGCTTCCGGCC 1293
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QY 1261 GGCAGTCCCAACCAAGTGCAGAAAGAGCTGAGCTTCAACGACCGAAACCCGCTTCCGGCC 1320
DB 1261 GGCAGTCCCAACCAAGTGCAGAAAGAGCTGAGCTTCAACGACCGAAACCCGCTTCCGGCC 1320
QY 1294 TCGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATGCTGACACAGCCCTTGGC 1353
DB 1294 TCGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATGCTGACACAGCCCTTGGC 1353
QY 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATGCTGACACAGCCCTTGGC 1380
DB 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATGCTGACACAGCCCTTGGC 1380
QY 1354 ACTGATGATGATATGATGAAAAAGAGTCCAGTGTGATGATGATGATGATGATGATGATGAT 1413
DB 1354 ACTGATGATGATATGATGAAAAAGAGTCCAGTGTGATGATGATGATGATGATGATGATGAT 1413
QY 1414 CCAACCACTTAAATCTGTCACTTGAAGTATCAAGATTTATGAAATTTGATGTTGCAAAAG 1473
DB 1414 CCAACCACTTAAATCTGTCACTTGAAGTATCAAGATTTATGAAATTTGATGTTGCAAAAG 1473
QY 1441 CCAACCACTTAAATCTGTCACTTGAAGTATCAAGATTTATGAAATTTGATGTTGCAAAAG 1500
DB 1441 CCAACCACTTAAATCTGTCACTTGAAGTATCAAGATTTATGAAATTTGATGTTGCAAAAG 1500
QY 1474 AAGTTAAGAAACGTTAGTGCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
DB 1474 AAGTTAAGAAACGTTAGTGCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
QY 1501 AAGTTAAGAAACGTTAGTGCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 AAGTTAAGAAACGTTAGTGCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1534 GGTCACTGGAATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
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QY 1561 GGTCACTGGAATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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QY 1594 GGAAGAGGCGAAATCATCATGATTAAGAAAGAGCGGAGAAATTAACAGCAAGCTGAG 1653
DB 1594 GGAAGAGGCGAAATCATCATGATTAAGAAAGAGCGGAGAAATTAACAGCAAGCTGAG 1653
QY 1621 GGAAGAGGCGAAATCATCATGATTAAGAAAGAGCGGAGAAATTAACAGCAAGCTGAG 1680
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QY 1654 ACCAGAGAGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1713
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QY 1681 ACCAGAGAGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 ACCAGAGAGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1714 ATGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTTCGAAAGGCTCT 1773
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QY 1741 ATGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTTCGAAAGGCTCT 1800
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QY 1774 GCTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1833
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QY 1801 GCTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
DB 1801 GCTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
QY 1834 GACTATCAAGGCTGTGATGCAAGAAAGATCTTTTGGGGTTCGCAAAAGAGTGGCTGC 1893
DB 1834 GACTATCAAGGCTGTGATGCAAGAAAGATCTTTTGGGGTTCGCAAAAGAGTGGCTGC 1893
QY 1861 GACTATCAAGGCTGTGATGCAAGAAAGATCTTTTGGGGTTCGCAAAAGAGTGGCTGC 1920
DB 1861 GACTATCAAGGCTGTGATGCAAGAAAGATCTTTTGGGGTTCGCAAAAGAGTGGCTGC 1920
QY 1894 TTATCCAGATCAATAGTCCCAACATCTGAGAGGCTGCAAGTCTTTCGACGCAAT 1953
DB 1894 TTATCCAGATCAATAGTCCCAACATCTGAGAGGCTGCAAGTCTTTCGACGCAAT 1953
QY 1921 TTATCCAGATCAATAGTCCCAACATCTGAGAGGCTGCAAGTCTTTCGACGCAAT 1980
DB 1921 TTATCCAGATCAATAGTCCCAACATCTGAGAGGCTGCAAGTCTTTCGACGCAAT 1980
QY 1954 GAGTCAAGTCCCAAGCTTTCTACGCGCTTACGCTTACCTATGATGATGATGATGATGATGAT 2013
DB 1954 GAGTCAAGTCCCAAGCTTTCTACGCGCTTACGCTTACCTATGATGATGATGATGATGATGAT 2013
QY 1981 GAGTCAAGTCCCAAGCTTTCTACGCGCTTACGCTTACCTATGATGATGATGATGATGATGAT 2040
DB 1981 GAGTCAAGTCCCAAGCTTTCTACGCGCTTACGCTTACCTATGATGATGATGATGATGATGAT 2040
QY 2014 GTGCAATTAAGTCAAGAGGATGCTCAGAGTGGGAGCCCAACCAATTCGAAACCA 2073
DB 2014 GTGCAATTAAGTCAAGAGGATGCTCAGAGTGGGAGCCCAACCAATTCGAAACCA 2073
QY 2041 GTGCAATTAAGTCAAGAGGATGCTCAGAGTGGGAGCCCAACCAATTCGAAACCA 2100
DB 2041 GTGCAATTAAGTCAAGAGGATGCTCAGAGTGGGAGCCCAACCAATTCGAAACCA 2100
QY 2074 ATTAATACGGCAACCAAGCAAGCCCAACCAATTTTCAAGATCCACTCTCCCA 2133
DB 2074 ATTAATACGGCAACCAAGCAAGCCCAACCAATTTTCAAGATCCACTCTCCCA 2133

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QY	2134	GCCATCAAGCATCTGCCCGAGGCGAGAAACTCTGCACTCTAACCTGCAAGGCTTACAGGAA	2193
Db	2161	GCCATCAAGCATCTGCCCGAGGCGAGAAACTCTGCACTCTAACCTGCAAGGCTTACAGGAA	2220
QY	2194	AGCATTTCTGACGTCAACCAACGCTGTTGTGCTCAAGGAAAAATGTTCAAGTTGACAG	2253
Db	2221	AGCATTTCTGACGTCAACCAACGCTGTTGTGCTCAAGGAAAAATGTTCAAGTTGACAG	2280
QY	2254	TCAATCTCACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGAGAGAGAAACTGTG	2313
Db	2281	TCAATCTCACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGAGAGAGAAACTGTG	2340
QY	2314	TTGTCTGTCTGTCCCATGTGTGCGGAGGAACTTTGTCTGTCTCAAAACCTG	2373
Db	2341	TTGTCTGTCTGTCCCATGTGTGCGGAGGAACTTTGTCTGTCTCAAAACCTG	2400
QY	2374	ATCAGGTGACCGAGGAACTGAATATACACTTTTCAGGAGTGAATCAAGTGTCTCAGA	2433
Db	2401	ATCAGGTGACCGAGGAACTGAATATACACTTTTCAGGAGTGAATCAAGTGTCTCAGA	2460
QY	2434	GGCAGCCCAAGATTTTATACCCCAATGAGGGAAATCCAAATGTTTATATACGTGAGAG	2493
Db	2461	GGCAGCCCAAGATTTTATACCCCAATGAGGGAAATCCAAATGTTTATATACGTGAGAG	2520
QY	2494	GTGGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGACCGCAGCCTGCCAGGGAA	2553
Db	2521	GTGGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGACCGCAGCCTGCCAGGGAA	2580
QY	2554	GCTGCTTTTGCATCAGACTCTTAAAGACTGGAAGTCAAGATCATCTCAAGACATTTGT	2613
Db	2581	GCTGCTTTTGCATCAGACTCTTAAAGACTGGAAGTCAAGATCATCTCAAGACATTTGT	2640
QY	2614	AAGGCAGAGAAATPACAGATGCCCTGACGTTGCTCATGTCCAAATGAAATPAA	2667
Db	2641	AAGGCAGAGAAATPACAGATGCCCTGACGTTGCTCATGTCCAAATGAAATPAA	2694

RESULT 11
US-09-813-148-1

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? Sequence 1, Application US/03813148
? Patent No. US20020076809A1
? GENERAL INFORMATION:
?
? APPLICANT: STEINMEYER, Klaus
? APPLICANT: LERCHE, Christian
? APPLICANT: SCHERER, Constanze
? APPLICANT: SEEBOM, Giscard
? APPLICANT: BUSCH, Andreas E.
? TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
? TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
? FILE REFERENCE: 38005-119
? CURRENT APPLICATION NUMBER: US/09/813,148
? CURRENT FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: DE 100 13 732.6
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: US 60/194,041
? PRIOR FILING DATE: 2000-04-03
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 1
? LENGTH: 3074
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-813-148-1

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Query Match	98.1%;	Score 2617.2;	DB 9;	Length 3074;
Best Local Similarity	98.7%;	Pred. No. 0;		
Matches 2659; Conservative	0;	Mismatches 8;	Indels 27;	Gaps 1

1 ATGAAGGATGTGTGAGTCTGGGGCCGGGGGCAGAGGGTGTCTGTGAATCTGGCAGCCCGCAGGGGC 60

[illegible]

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QY 1116 --TCAGAGCTAAGTTTAAAGAGCGAGTGCATGGCTAGCCCAAGGGGCCAGAGATT 1173
 DB 1355 AGTCAGAGCTAAGTTTAAAGAGCGAGTGCATGGCTAGCCCAAGGGGCCAGAGATT 1414
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 DB 1415 AAGAGCCGACAGCTCAGTAGTGAAGAGGTCCTCCCAAGCAACGACATCACAGCCGAG 1474
 QY 1234 GGCAGTCCCAAGAGTGAAGAGTGCATGGCTAAGAGCCGAGCCGCTCCGCCCC 1293
 DB 1475 GGCAGTCCCAAGAGTGAAGAGTGCATGGCTAAGAGCCGAGCCGCTCCGCCCC 1534
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 DB 1535 TCGCTCGCTCAAAAAGTTCTCAGCCCAAAACAGTGTATAGTCTGACACAGCCCTGGC 1594
 QY 1354 ACTGATGATGTATATGATGAAAAAGATGCGCAGTGTATATCAGTGAAAGCTTCACC 1413
 DB 1595 ACTGATGATGTATATGATGAAAAAGATGCGCAGTGTATATCAGTGAAAGCTTCACC 1654
 QY 1414 CCACCACTTAAACCTGCTATGAGCTATCAGAAATTATGAAATTTGATGTTGAAAAACGG 1473
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 DB 1835 GGAAAGGGGCAATTCATCAGATTAAGAAAGCGGAGAAATTAACAGAGAACTGAG 1894
 QY 1654 ACCACAGAGATCTCAGTATGCTCGGTGCTGCTCAAGGTTGAAAAACAGTACAGTGC 1713
 DB 1895 ACCACAGAGATCTCAGTATGCTCGGTGCTGCTCAAGGTTGAAAAACAGTACAGTGC 1954
 QY 1714 ATAGAGTCCAGGTGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGAAAGGCTCT 1773
 DB 1955 ATAGAGTCCAGGTGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGAAAGGCTCT 2014
 QY 1774 GCTCAGCCCTCGCTTGGCTTCAATCCAGATTCCTCAACCTTTTGAATGTGAACAGATCT 1833
 DB 2015 GCTCAGCCCTCGCTTGGCTTCAATCCAGATTCCTCAACCTTTTGAATGTGAACAGATCT 2074
 QY 1834 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAAAGTGGCTGC 1893
 DB 2075 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAAAGTGGCTGC 2134
 QY 1894 TTATCCAGATCAATAGTGCACCAATCTCGAGAGGCTCGAGTTCACTTCTGAGCCCAAT 1953
 DB 2135 TTATCCAGATCAATAGTGCACCAATCTCGAGAGGCTCGAGTTCACTTCTGAGCCCAAT 2194
 QY 1954 GAGTTCAAGTCCCAAGCTTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACAG 2013
 DB 2195 GAGTTCAAGTCCCAAGCTTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACAG 2254
 QY 2014 GTGCCAAATTAAGTCAAAAGCATGGCTCAGAGTGGAGCCCAACCAACATTTGCAACCAA 2073
 DB 2255 GTGCCAAATTAAGTCAAAAGCATGGCTCAGAGTGGAGCCCAACCAACATTTGCAACCAA 2314
 QY 2074 ATTAATATCGGCAACCAAGCCAGCAAGCCCAACCAATTTTACAGATCCACCTCTCTCCA 2133
 DB 2315 ATTAATATCGGCAACCAAGCCAGCAAGCCCAACCAATTTTACAGATCCACCTCTCTCCA 2374
 QY 2134 GGCATCAAGCATCTGCGCAGGCGCAAGAAATCTGCAACCTTCAAGAGCTTTACAGAA 2193
 DB 2375 GGCATCAAGCATCTGCGCAGGCGCAAGAAATCTGCAACCTTCAAGAGCTTTACAGAA 2434

QY 2194 AGCATTTCTGACGTCCACCACTGCTTGTGTGCTCCAAAGAAATGTTCAGTTGACAG 2253
 DB 2435 AGCATTTCTGACGTCCACCACTGCTTGTGTGCTCCAAAGAAATGTTCAGTTGACAG 2494
 QY 2254 TCAATCTCAACCAAGGACCGTTCTATGAGAAAAAGTTTGAACATGGAGAGAACTCTG 2313
 DB 2495 TCAATCTCAACCAAGGACCGTTCTATGAGAAAAAGTTTGAACATGGAGAGAACTCTG 2554
 QY 2314 TTGTCTGTGTCCTCCATGGTGCAGAAAGCATTTGGGCAATCTTTGTCTGTGCAAAACCTG 2373
 DB 2555 TTGTCTGTGTCCTCCATGGTGCAGAAAGCATTTGGGCAATCTTTGTCTGTGCAAAACCTG 2614
 QY 2374 ATCAGGTCCAGCGAGAACTGAATATACACTTTTCAGGAGTGAAGTCAAGTGGCTCAGA 2433
 DB 2615 ATCAGGTCCAGCGAGAACTGAATATACACTTTTCAGGAGTGAAGTCAAGTGGCTCAGA 2674
 QY 2434 GGCAGCAAGATTTTATCCCAATGAGAGGAAATCCAAATGTTTATTAACATGAAAGAG 2493
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 QY 2494 GTGGGTCCGGAAGAGACAGAGACAGACACTTTTGAATGCGCACCGGAGCTGCCAGGAA 2553
 DB 2735 GTGGGTCCGGAAGAGACAGAGACAGACACTTTTGAATGCGCACCGGAGCTGCCAGGAA 2794
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 DB 2855 AAGCAGAGAAAGTACAGATGCTCCCTCAGCTTGCCTCATGTCAAACTGAATTA 2908

RESULT 12
 US-10-399-489A-5
 ; Sequence 5, Application US/10399489A
 ; Publication No. US2005010104A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: ARGENTIERI, Thomas M.
 ; APPLICANT: SHELDON, Jeffrey H.
 ; TITLE OF INVENTION: METHODS OF SELECTING COMPOUNDS FOR MODULATION OF BLADDER FUNCTION
 ; FILE REFERENCE: AML00620
 ; CURRENT APPLICATION NUMBER: US/10/399,489A
 ; PRIORITY FILING DATE: 2003-04-17
 ; PRIOR APPLICATION NUMBER: 60/241,078
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: PCT/US01/32371
 ; PRIOR FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 60/281,428
 ; PRIOR FILING DATE: 2001-04-04
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patencin version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 3074
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-399-489A-5

Query Match 98.1%; Score 2617.2; DB 21; Length 3074;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;
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 DB 215 ATGAAGATGTGAGTCCGCGCCGAGGCTGCTGCTGAACTCGGACGCGCCAGGGC 274
 QY 61 GACGCGCTGCTACCTGCTGGGACCCGCGCGGACACGTTGATGGCGGGGCGGCGCTG 120
 DB 275 GACGCGCTGCTACCTGCTGGGACCCGCGCGGACACGTTGATGGCGGGGCGGCGCTG 334
 QY 121 AGGAGAGCCGCGCGGAGCAAGCAAGGAGCCCGGATGAGCTGCTGGGAAAGCGCTCTT 180

335 AGGAGAGCCGCCGGGCAAGACAGGGGAGCCGAGTAGCCTGCTGGAAAGCCGCTCTCT 394
181 TACAGAGTAGCCAGAGCTGCGGCGCAACGTCAGATACCGGCGGGTGGAGAACTACTG 240
395 TACACGAGTAGCCAGAGCTGCGGCGCAACGTCAGATACCGGCGGGTGGAGAACTACTG 454
241 TACAAAGTCTGGAGAGAGACCCCGGCGGCTGGGCTTATCATCAACGCTTTCGTTTTCTC 300
455 TACAAAGTCTGGAGAGAGACCCCGGCGGCTGGGCTTATCATCAACGCTTTCGTTTTCTC 514
301 CTGTCCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
515 CTGTCCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 574
361 GCCTCAAGTGGCTCTTGAATCTGAGATTGCTGATGATGCTGCTCTTGGTGGAGTTTC 420
575 GCCTCAAGTGGCTCTTGAATCTGAGATTGCTGATGATGCTGCTCTTGGTGGAGTTTC 634
421 ATCATTCGAATCTGATCTGCTGCGGGTCTGTTGTCGATATAGAGATGCAAGAGACTG 480
635 ATCATTCGAATCTGATCTGCTGCGGGTCTGTTGTCGATATAGAGATGCAAGAGACTG 694
481 AGGTTGGCTGAAAGCCCTTCTGTTATAGATACCATGTTCTTATGCTTCAATAGCA 540
695 AGGTTGGCTGAAAGCCCTTCTGTTATAGATACCATGTTCTTATGCTTCAATAGCA 754
541 GTTGTCTTGGCAAAAACCTCAGGGTAATATTTTGGCAGCTCTGCACTCAGAAATCTCG 600
755 GTTGTCTTGGCAAAAACCTCAGGGTAATATTTTGGCAGCTCTGCACTCAGAAATCTCG 814
601 TTCTCAGATCTCTCCGATGCTGCGCATGAGACCGAAGGGAGGCACTTGGAAATTAATG 660
815 TTCTCAGATCTCTCCGATGCTGCGCATGAGACCGAAGGGAGGCACTTGGAAATTAATG 874
661 GGTTCAGTGGTTATGCTCAGACAGAGAAATTAATCAGCTTGGTATGATAGATTTTGG 720
875 GGTTCAGTGGTTATGCTCAGACAGAGAAATTAATCAGCTTGGTATGATAGATTTTGG 934
721 GTTCTTATTTTTCGTCCTTCTCTTCTATCTGCTGGAAGAGATGCCAATAAGAGTTT 780
935 GTTCTTATTTTTCGTCCTTCTCTTCTATCTGCTGGAAGAGATGCCAATAAGAGTTT 994
781 TCTACATATGAGATGCTCTCTGCTGGGGCACAATTAATGCAACTATTTGGCTATGGA 840
995 TCTACATATGAGATGCTCTCTGCTGGGGCACAATTAATGCAACTATTTGGCTATGGA 1054
841 GACAAAACCTCCCTAATCTGGCTGGGGAAGATGCTTTCGCAAGGCTTTCACCTCTGGC 900
1055 GACAAAACCTCCCTAATCTGGCTGGGGAAGATGCTTTCGCAAGGCTTTCACCTCTGGC 1114
901 ATTTCTTCTTGGCACTTCTCTGCGGCAATTCCTGCTCAGATTTTTCATTTAAAGTACA 960
1115 ATTTCTTCTTGGCACTTCTCTGCGGCAATTCCTGCTCAGATTTTTCATTTAAAGTACA 1174
961 GAAACAACCCCGGCAAGAACCTTTGAGAAAGAGAACCCAGCTGCCAATCTCATTCAG 1020
1175 GAAACAACCCCGGCAAGAACCTTTGAGAAAGAGAACCCAGCTGCCAATCTCATTCAG 1234
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1235 TGGTGGTGGGATAGTACGAGAGCTGATGAGAAATCTGTTTCACTTTCAGCTGGAGGCA 1294
1081 CACTTGAAGGCTTGGACACTTGCAGCCCTACCA----- 1115
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1116 --TCAGAGCTAAGTTTAAAGAGCAAGTGCATGAGTACCCCAAGGGGCCAGAGTATT 1173
1355 AGTCAAGAGCTAAGTTTAAAGAGCAAGTGCATGAGTACCCCAAGGGGCCAGAGTATT 1414
1174 AAGAGCGCAAGAGCTCAGAGGTGACAGAGGTCCCAAGCAAGCAATCAACGCGAG 1233
1415 AAGAGCGCAAGAGCTCAGAGGTGACAGAGGTCCCAAGCAAGCAATCAACGCGAG 1474

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1475 GGCAGTCCCAACCAAGTGCAGAGAGTGAAGCTTCAACGACCCGACCCGCTTCCGGCCC 1534
1294 TCGCTGCGCCTTCAAAAGTTTCTCAGCCAAACCAAGATAGATGCTGACACAGCCTTGGC 1353
1535 TCGCTGCGCCTTCAAAAGTTTCTCAGCCAAACCAAGATAGATGCTGACACAGCCTTGGC 1594
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1595 ACTGATGATGATATGATGAGAAAGAGATGCCAGTGTGATGATATCAGTGAAGACCTCAC 1654
1414 CCACCACTTAAACCTGTCATTCAGACTATCAGAAATTAATGAAATTTTCACTTGCAGAAC 1473
1655 CCACCACTTAAACCTGTCATTCAGACTATCAGAAATTAATGAAATTTTCACTTGCAGAAC 1714
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1955 ATAGAGTCCAAGCTGGAATGCTGCTACTAGACATCTATCAACAGTCTCTCGAAAGGCTCT 2014
1774 GCTCAGCCTTGCCTTGGCTTCAATTCAGATCCACCTTTTGAATGGAACAGACATCT 1833
2015 GCTCAGCCTTGCCTTGGCTTCAATTCAGATCCACCTTTTGAATGGAACAGACATCT 2074
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2075 GACTATCAAAAGCCCTGATGATAGCAAAAGATCTTTCGGGCTCCGCAAAACAGTGGCTC 2134
1894 TTATCAGATCAACTAGTGCACCAACTCTCGAGAGGCTGCAAGTTTATCTGACGCAAT 1953
2135 TTATCAGATCAACTAGTGCACCAACTCTCGAGAGGCTGCAAGTTTATCTGACGCAAT 2194
1954 GAGTTCAGTCCGACACTTTCACGCGCTTACGCTTACCTTACATGACAGTCAACCAACAG 2013
2195 GAGTTCAGTCCGACACTTTCACGCGCTTACGCTTACCTTACATGACAGTCAACCAACAG 2254
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2255 GTGCCAATTAATGCAAGAGTGCCTCAGCAGTGGAGGCAACCAACCAATTCGCAACCA 2314
2074 ATAAATTAAGGCAACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2133
2315 ATAAATTAAGGCAACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2374
2134 GGCATCAAGCATCTGCGCAGGCAAGAACTGCAACCTTACAGGCTTACAGGAA 2193
2375 GGCATCAAGCATCTGCGCAGGCAAGAACTGCAACCTTACAGGCTTACAGGAA 2434
2194 AGCATTTTTCAGAGTCAACCACTGCTTGTGCTTCAAGGAAATGTTCAAGGTTCACAG 2253
2435 AGCATTTTTCAGAGTCAACCACTGCTTGTGCTTCAAGGAAATGTTCAAGGTTCACAG 2494
2254 TCAATTCACCAAGAGCCGTTCTATGAGAGAAACCTTTCAGATGAGAGAGAACTCTG 2313
2495 TCAATTCACCAAGAGCCGTTCTATGAGAGAAACCTTTCAGATGAGAGAGAACTCTG 2554

QY 2314 TTGCTGTCTGTCATGTCGCGAAGAGCTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2373
DB 2555 TTGCTGTCTGTCATGTCGCGAAGAGCTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2614
QY 2374 ATCAGGTGCGACCGAAGAACTGAATATACAACTTTACAGGAGTGAAGTCAAGTGTGCTCCAGA 2433
DB 2615 ATCAGGTGCGACCGAAGAACTGAATATACAACTTTACAGGAGTGAAGTCAAGTGTGCTCCAGA 2674
QY 2434 GGCAGCCAAATTTTAACTCCCAATGAGGGAATCCAAATTTGTTTAACTGAATGAAGAG 2493
DB 2675 GGCAGCCAAATTTTAACTCCCAATGAGGGAATCCAAATTTGTTTAACTGAATGAAGAG 2734
QY 2494 GTGGGTCCCGAAGAGACAGAGACGACCTTTTGTATGTCGACCGACGCTGCGACGGA 2553
DB 2735 GTGGGTCCCGAAGAGACAGAGACGACCTTTTGTATGTCGACCGACGCTGCGACGGA 2794
QY 2554 GCTGCTTTTGATCAGACTCTCTTAAGAGCTGAAAGGTCAAGATCATCTCAGACATTTGT 2613
DB 2795 GCTGCTTTTGATCAGACTCTCTTAAGAGCTGAAAGGTCAAGATCATCTCAGACATTTGT 2854
QY 2614 AAGGCAAGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAATAA 2667
DB 2855 AAGGCAAGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAATAA 2908

RESULT 13

US-10-482-834A-55
Sequence 55, Application US/10482834A
Publication No. US2005007476A1
GENERAL INFORMATION:
APPLICANT: Mulley, John Charles
APPLICANT: Harlin, Louise Anne
APPLICANT: Dibiens, Michelle
APPLICANT: Wallace, Robyn
APPLICANT: Phillips, Hillary Amy
APPLICANT: Heron, Sara Elizabeth
APPLICANT: Berkovic, Samuel Frank
APPLICANT: Scheffer, Ingrid Eileen
APPLICANT: Biomedica Limited
TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
FILE REFERENCE: 1386/17
CURRENT APPLICATION NUMBER: US/10/482,834A
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-10-482-834A-55

Query Match 98.1%; Score 2615.6; DB 21; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2658; Conservative 0; Mismatches 9; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGAGTCCGGGCGGAGGAGTGTCTGTGAATCGGACGCGCAGGAGG 60
DB 215 ATGAAGATGTGAGTCCGGGCGGAGGAGTGTCTGTGAATCGGACGCGCAGGAGG 274
QY 61 GACGCGCTGTCTGTGAGCACCGCGCGGACGCTGTGTGCGCGCGGCTGTGCTG 120
DB 275 GACGCGCTGTCTGTGAGCACCGCGCGGACGCTGTGTGCGCGCGGCTGTGCTG 334
QY 121 AAGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 335 AAGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 394
QY 181 TACACAGTAGCAGAGCTGCGCGCAGAGCTCAAGTACCGGCGGAGTGAAGTCACTG 240
DB 395 TACACAGTAGCAGAGCTGCGCGCAGAGCTCAAGTACCGGCGGAGTGAAGTCACTG 454
QY 241 TACACAGTAGCAGAGCTGCGCGCAGAGCTCAAGTACCGGCGGAGTGAAGTCACTG 300

DB 455 TACACAGTAGCAGAGCTGCGCGCAGAGCTCAAGTACCGGCGGAGTGAAGTCACTG 514
QY 301 CTGTGCTTTGGTGTGCTGATTTTGTGAGTGTCTTCAACATCCCTAGAGACAAATTTG 360
DB 515 CTGTGCTTTGGTGTGCTGATTTTGTGAGTGTCTTCAACATCCCTAGAGACAAATTTG 574
QY 361 GCCTCAAGTTGCTCTTGAATCCGAGTGTGATGATGATGATGATGATGATGATGATG 420
DB 575 GCCTCAAGTTGCTCTTGAATCCGAGTGTGATGATGATGATGATGATGATGATGATG 634
QY 421 ATCATTGATCTGTGTCGCGGAGTGTGTGTGATATAGAGATGAGAGAGAGAGAGAG 480
DB 635 ATCATTGATCTGTGTCGCGGAGTGTGTGTGATATAGAGATGAGAGAGAGAGAGAG 694
QY 481 AGTTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 540
DB 695 AGTTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 754
QY 541 GTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 600
DB 755 GTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 814
QY 601 TTCTTACAGATCTCTCGCATGTGTGCGATGACCGAAGGAGAGGACCTTGAATTTAGT 660
DB 815 TTCTTACAGATCTCTCGCATGTGTGCGATGACCGAAGGAGAGGACCTTGAATTTAGT 874
QY 661 GTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 720
DB 875 GTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 934
QY 721 GTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 780
DB 935 GTTGTGTCGAGAGGCTTGTGTGTATATAGATATCATTTGTTTCCCTTCAATAGA 994
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DB 1235 TGTGTTTGGCTGATTTAGGAGAGTGTGAGAAATCTGTTTCCATTGCAACTGGAAGCA 1294
QY 1081 CACTTGAAGGCTTGTGACACTGACGCTTACCA----- 1115
DB 1295 CACTTGAAGGCTTGTGACACTGACGCTTACCA----- 1354
QY 1116 --TCAGAGCTTAAGTTTAAAGAGGAGTGTGCGATGTGAGCCAGGCGGAGATAT 1173
DB 1355 AGTCAGAGCTTAAGTTTAAAGAGGAGTGTGCGATGTGAGCCAGGCGGAGATAT 1414
QY 1174 AAGAGCCGACCAAGCTCTGATGATGACAGAGAGTCCCAAGACCGACATCAAGCCGAG 1233
DB 1415 AAGAGCCGACCAAGCTCTGATGATGACAGAGAGTCCCAAGACCGACATCAAGCCGAG 1474
QY 1234 GGCAGTCCCAAGAGTGTGAGAGAGTGTGAGAGCTTCAAGACCGAGCCGCTTCCGCGCC 1293
DB 1475 GGCAGTCCCAAGAGTGTGAGAGAGTGTGAGAGCTTCAAGACCGAGCCGCTTCCGCGCC 1534
QY 1294 TCGCTGCGCTCAAAAGTTTCTGAGCAAAACCAAGTATGATGCTGACACAGCCCTTGGC 1353
DB 1535 TCGCTGCGCTCAAAAGTTTCTGAGCAAAACCAAGTATGATGCTGACACAGCCCTTGGC 1594

OY	1354	ACTGATGATGATATGAGAAAAAGAGCCGAGTGTGATGATCAGTGGAAAGACCTCAC	1413
Db	1595	ACTGATGATGATATGATGAAAAAGATGCCAGTGTGATGATCAGTGGAAAGACCTCAC	1654
OY	1414	CCACCACCTTAAAACTGTCATTTCGAGCTATCAGAAATTATGAAATTTGATGTGGCAAA	1473
Db	1655	CCACCACCTTAAAACTGTCATTTCGAGCTATCAGAAATTATGAAATTTGATGTGGCAAA	1714
OY	1474	AAAGTTAAGGAAACGTTACGTCGCATATGATATGTAAGAAAGATGTCATGGAACAATA	1533
Db	1715	AAAGTTAAGGAAACGTTACGTCGCATATGATATGTAAGAAAGATGTCATGGAACAATA	1774
OY	1534	GGTCATCTGGAACATGTTGTGTGATGAATTTAAAAAGCTTTCAAAGACGTTGATCAAA	1593
Db	1775	GTCATCTGGAACATGTTGTGTGATGAATTTAAAAAGCTTTCAAAGACGTTGATCAAA	1834
OY	1594	GGAAAAAGGGCAAAATACATCAAGTATGAAGAGCCGAGAGAAAAATTAACGCGAACA	1653
Db	1835	GGAAAAAGGGCAAAATACATCAAGTATGAAGAGCCGAGAGAAAAATTAACGCGAACA	1894
OY	1654	ACCAACAGACGATCTCAGATGCTCGGTGGGGTGTCAAGGTGTGAAAAACAAGTACAG	1713
Db	1895	ACCAACAGACGATCTCAGATGCTCGGTGGGGTGTCAAGGTGTGAAAAACAAGTACAG	1954
OY	1714	ATPAGATCCAAAGTGTGACTGCTGCTTACAGACATCTATCAACAGGTCTTTGAAAA	1773
Db	1955	ATPAGATCCAAAGTGTGACTGCTGCTTACAGACATCTATCAACAGGTCTTTGAAAA	2014
OY	1774	GGCTCAGCCCTCGGCTTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGAC	1833
Db	2015	GGCTCAGCCCTCGGCTTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGAC	2074
OY	1834	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGGGGTTCGCACAAAACAGTGG	1893
Db	2075	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGGGGTTCGCACAAAACAGTGG	2134
OY	1894	TTATTCAGATCAACTAGTGGCCAACTCTCGAGAGGCCCTGCAAGTTGATTTCTGACG	1953
Db	2135	TTATTCAGATCAACTAGTGGCCAACTCTCGAGAGGCCCTGCAAGTTGATTTCTGACG	2194
OY	1954	GAGTTCAAGTCCAGACCTTCTTACGCGGTTTAGCCCTTATGSCAGTCAAGCAACAG	2013
Db	2195	GAGTTCAAGTCCAGACCTTCTTACGCGGTTTAGCCCTTATGSCAGTCAAGCAACAG	2254
OY	2014	GTGCCAATTAGTCAAAAGCGATGCTCAGAGGTGCGACCCACCAACCATTTGGCAAC	2073
Db	2255	GTGCCAATTAGTCAAAAGCGATGCTCAGAGGTGCGACCCACCAACCATTTGGCAAC	2314
OY	2074	ATTAATATAGGAGACCCAGCAAGCCAGGCCCCCAACCTTTACAGATCCCACTCTCT	2133
Db	2315	ATTAATATAGGAGACCCAGCAAGCCAGGCCCCCAACCTTTACAGATCCCACTCTCT	2374
OY	2134	GCCATCAAGACATTTGCCAGGCGCAGAAACTCTGACCCCTAACCTCTGACGGCTT	2193
Db	2375	GCCATCAAGACATTTGCCAGGCGCAGAAACTCTGACCCCTAACCTCTGACGGCTT	2434
OY	2194	AGCATTTCTGACGTCAACCACTGCTTTGTGCTCTCAAGAGAAATGTTCAAGTTGCA	2253
Db	2435	AGCATTTCTGACGTCAACCACTGCTTTGTGCTCTCAAGAGAAATGTTCAAGTTGCA	2494
OY	2254	TCAAAATCTCAACCAAGGACCGTTCTTATGAGAAAAAGCTTTGACATGGAGAGAA	2313
Db	2495	TCAAAATCTCAACCAAGGACCGTTCTTATGAGAAAAAGCTTTGACATGGAGAGAA	2554
OY	2314	TTGTCTGTCTGTCCCATGTGTGCGAAGGACTTGGGCAAAATCTTTGTCTGTGCAAA	2373
Db	2555	TTGTCTGTCTGTCCCATGTGTGCGAAGGACTTGGGCAAAATCTTTGTCTGTGCAAA	2614
OY	2374	ATCAGGTGACCGAGGAACGTGAATTACACTTTTACAGGAGTGAAGTCAAGGTGCT	2433
Db	2615	ATCAGGTGACCGAGGAACGTGAATTACACTTTTACAGGAGTGAAGTCAAGGTGCT	2674

QY	2434	GGAGCCCAAGATTTTAACTCCCAAAATGAGGAAATCAAAATTTGTTATTAATGATGAAG	2493
Db	2675	GGAGCCCAAGATTTTAACTCCCAAAATGAGGAAATCAAAATTTGTTATTAATGATGAAG <td>2734</td>	2734
QY	2494	GTGGGTCCCGAAGAGACAGAGACACACTTTTGTATGCGCACCGACGCTCCAGGGAA	2553
Db	2735	GTGGGTCCCGAAGAGACAGAGACACACTTTTGTATGCGCACCGACGCTCCAGGGAA	2794
QY	2554	GCTGCTTTTGATCAGACTCTCTTAAGAGACTGGAAAGGTCAAGATCATCTCAGAGCATTTGT	2613
Db	2795	GCTGCTTTTGATCAGACTCTCTTAAGAGACTGGAAAGGTCAAGATCATCTCAGAGCATTTGT	2854
QY	2614	AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATATA	2667
Db	2855	AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATATA	2908
RESULT 14			
US-10-313-542-303			
Sequence 303, Application US/10313542			
Publication No. US20030120057A1			
GENERAL INFORMATION:			
APPLICANT: Rooda, Reddy			
APPLICANT: Guejier, Karl, J.			
APPLICANT: Au-Toung, Janice			
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED PR			
FILE REFERENCE: PA-0013 US			
CURRENT FILING DATE: 2002-12-05			
PRIOR FILING DATE: 2000-01-31			
PRIOR APPLICATION NUMBER: US/09/495,050			
PRIOR FILING DATE: 1999-02-01			
NUMBER OF SEQ ID NOS: 305			
SOFTWARE: PERL Program			
SEQ ID NO 303			
LENGTH: 582			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc feature			
OTHER INFORMATION: Incyte ID No. US20030120057A1 4970006CT1			
US-10-313-542-303			
Query Match	19.1%	Score 509.8;	DB 15; Length 582;
Best Local Similarity	99.4%;	Pred. No. 2.3e-146;	Indels 1; Gaps 1;
Matches 522; Conservative	0;	Mismatches	
QY	1594	GGAAAAAGGCAAAATACATCAGATTAAGAAGACCGAGAGAAATTAACAGACAAATGAG	1653
Db	1	GGAAAAAGGCAAAATACATCAGATTAAGAAGACCGAGAGAAATTAACAGACAAATGAG	60
QY	1654	ACCACAGACGATTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGTACAGTCC	1713
Db	61	ACCACAGACGATTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGTACAGTCC	120
QY	1714	ATAGAGTCCAAAGCTGAGACTGCTACTAGACATCTATCAACAGGTCTTGGAAAGGCTCT	1773
Db	121	ATAGAGTCCAAAGCTGAGACTGCTACTAGACATCTATCAACAGGTCTTGGAAAGGCTCT	180
QY	1774	GCTTCAGCCCTCGCTTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT	1833
Db	181	GCTTCAGCCCTCGCTTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT	240
QY	1834	GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTTGGGGTTCCGCAAAAACATGTGCTGC	1893
Db	241	GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTTGGGGTTCCGCAAAAACATGTGCTGC	300
QY	1894	TTATCCAGATCAACTAGTGCACAAATCTCGAAGAGGCTCGAGTTCAATTTGACGCGCAAT	1953
Db	301	TTATCCAGATCAACTAGTGCACAAATCTCGAAGAGGCTCGAGTTCAATTTGACGCGCAAT	360
QY	1954	GAGTTCAAGTCCCAAGACTTTTACGGCGCTTACGCTTACTATGCAAGTCAAGCAACACAG	2013

QY 1195 GGTGACAGGAGGTCCCAAGACATCACAGCCGAGG---GCAGTCCACCAAGTG 1251
DB 1460 ACAATCCCACTCCCAAGACGAGCAGGTGGTGAAGGCCACAGCCCAACCAAGTG 1519
QY 1252 CAGAGAGCTGAGGCTTCAACGACGACCCGCTTCCGGCCCTGCTGCGCTCAAAAGT 1311
DB 1520 CAAMAGGCTGAGGTCAATGACCCGACCCGCTTCCGGGCATCTTGAGACTC----- 1573
QY 1312 TCTCAGCCAAACCAAGTAGATGCTGACAGCCCTTGCACTGATGATGATATGAT 1371
DB 1574 -----AAACCCCGCACTCTGCTGAGAGTCCC---CTCAGAGAAAGTAGCAGAG 1621
QY 1372 GAAAAAGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1431
DB 1622 GAGAAAGAGCTACAGAGTGTGAGTCAAGGTGAGACATGATGATGATGATGATGATGAT 1681
QY 1432 ATTGAGCTATCAAGATTATGAATTTGATGTTGCAAAACGAAAGTTTAAAGAAAGTTA 1491
DB 1682 ATCCGCTCATGAGATTCTCAAGTTCCTGAGGCCCAAAAGAAATTCAAGAGACACTG 1741
QY 1492 CGTCATATGATGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1551
DB 1742 CGACCTAGACGCTGAAGAGAGTCAATTTGAGAGTACTCAGCAGGCCAAGCTGAGATGCTG 1801
QY 1552 TGTAGATTAAAGCCTTCAACACGCTGTGATCAAAATTTCTGAAAAAGGC---AAATC 1608
DB 1802 GGGCGGATCAAGAGCTGCAAACTCGGATGAGACAAATTTGTGGTGGGGGCCCGGGGAGC 1861
QY 1609 ACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAGAAATGAGACACAGACATCTC 1668
DB 1862 AGAAGGCCCGGGAGAGGGGCGACAAAGGGCCCTCCGACCGAGAGGTGGTGAATGAAATC 1921
QY 1669 AGTATGCTCGTGGGTGGTCAAGGTTGAAGAAAAAGGTAAGTCAATGAGTCAAGCTG 1728
DB 1922 AGCATATGAGAGCGCTGGTCAAGGTGAGAGAGAGTGAATGATGATGATGATGATGATG 1981
QY 1729 GACTGCTTAAGACATCTATCAACAGGTCTTGGAAAAAGGCTCTGAGCCCTGCT 1788
DB 1982 GACTGCTGTGGGCTTCTATTGCGGCTGCTGC-----GCTTGGCACTCGGCCAGC 2035
QY 1789 TTGGCTTCATTCAGATCCCACTTTGAAATGGAACAGACATCTGATCAAAAGCCT 1848
DB 2036 CTGGGGCGGTGCAAGTGCCTGTTGACCCGACATCACTCCGATTAACCAAGCCT 2095
QY 1849 GTGATAGCAAGATCTTGGGTTCCGCAAAA 1882
DB 2096 GTGAGCACGAGACATCTCTGCTCGCACAGA 2129

Search completed: October 23, 2005, 19:13:17
Job time : 1378.34 secs